

OM protein - protein search, using sw model
Run on: April 26, 2006, 17:43:36 ; Search time 140 Seconds
(without alignments)
979.187 Million cell updates/sec

Title: US-10-785-607C-9
Perfect score: 1605
Sequence: 1 MARSRRLRLLLRLVLA.....TFVLPALWKAAGSGRQGF 312
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 43937871 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	AA23324	standard; protein; 312 AA.		
DE	A33	related antigen PRO245.		
PN	WO327098-A2.			
PD	03-JUN-1999.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1605; DB 2;	Length 312;	
Best Local Similarity	100.0%;	Pred. No. 5.2e-123;		
RESULT 2				
ID	AA70860	standard; protein; 312 AA.		
DE	Human PRO245 protein.			
PN	WO914241-A2.			
PD	25-MAR-1999.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1605; DB 2;	Length 312;	
Best Local Similarity	100.0%;	Pred. No. 5.2e-123;		
RESULT 3				
ID	AA13354	standard; protein; 312 AA.		
DE	Amino acid sequence of protein PRO245.			
PN	WO9914328-A2.			
PD	25-MAR-1999.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1605; DB 2;	Length 312;	
Best Local Similarity	100.0%;	Pred. No. 5.2e-123;		
RESULT 4				
ID	AAB33421	standard; protein; 312 AA.		
DE	Human PRO245 protein UNQ219 SEQ ID NO:36.			
PN	WO200053758-A2.			
PD	14-SEP-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1605; DB 2;	Length 312;	
Best Local Similarity	100.0%;	Pred. No. 5.2e-123;		
RESULT 5				
ID	AA70668	standard; protein; 312 AA.		
DE	Human PRO245 protein.			
PN	WO200015797-A2.			
PD	23-MAR-2000.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1605; DB 3;	Length 312;	
Best Local Similarity	100.0%;	Pred. No. 5.2e-123;		
RESULT 6				
ID	AAB24401	standard; protein; 312 AA.		
DE	Human PRO245 protein sequence SEQ ID NO:67.			

PN WO20032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 7
ID ADC78384 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 8
ID AAB80222 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 9
ID AAU00821 standard; protein; 312 AA.
DE Human immune response protein PRO245 (UNQ219).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 10
ID AAU12339 standard; protein; 312 AA.
DE Human PRO245 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 11
ID AAB53081 standard; protein; 312 AA.
DE Human angiogenesis-associated protein PRO245, SEQ ID NO:91.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 12
ID ABU71600 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 13
ID ABO17783 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 14
ID ABU71455 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 15
ID ABU81037 standard; protein; 312 AA.
DE Human PRO polypeptide #169.
PN US2003004311-A1.

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PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 16
ID ABU17901 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 17
ID AB001784 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 18
ID ABU66737 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 19
ID ABU54357 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 20
ID AB047372 standard; protein; 312 AA.
DE Human secreted/transmembrane polypeptide PRO245.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 21
ID ABU59818 standard; protein; 312 AA.
DE Novel secreted and transmembrane protein PRO245.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 22
ID AB025008 standard; protein; 312 AA.
DE Human secreted/transmembrane protein (PRO) #168.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 23
ID ABU64509 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 24
ID ABU67355 standard; protein; 312 AA.
DE Human secreted protein PRO245.
PN US200302054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 25
ID ABO14875 standard; protein; 312 AA.
DE Human secreted / transmembrane polypeptide PRO245.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 26
ID ABU07738 standard; protein; 312 AA.
DE Human A-33 related antigen PRO245.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 27
ID ABU67013 standard; protein; 312 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 336.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 28
ID ABU69632 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 29
ID ABO14814 standard; protein; 312 AA.
DE Human secreted / transmembrane polypeptide PRO245.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 30
ID ADA45855 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 31
ID ADA76286 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 32
ID ADB29269 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 33
ID ADA18936 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 34
ID ADA61559 standard; protein; 312 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 35
ID ADB19344 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 36
ID ADB27885 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 37
ID ADA83664 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 38
ID ADB15928 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 39
ID ADA47714 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 40
ID ADA18125 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 41
ID ABO32766 standard; protein; 312 AA.
DE Human secreted/transmembrane protein PRO245.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 42
ID ADA67509 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;

Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 43
ID ADB30516 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 44
ID ADA85812 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 45
ID ADA97024 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 46
ID ADA79328 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 47
ID ADA87467 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 48
ID ADB16669 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 49
ID ABO34826 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 50
ID ADA16100 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 51
ID ADA91761 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;

RESULT 52
ID ADB14824 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 53
ID ADB18785 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 54
ID ADA94000 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 55
ID ADB19896 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 56
ID ADB13208 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 57
ID ABO43316 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 58
ID ADA74462 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 59
ID ADA42245 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 60
ID ADB24695 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 61
ID ADB25255 standard; protein; 312 AA.

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ID ADA82219 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 62
ID ADA75182 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 63
ID ADA85260 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 64
ID ADA84708 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 65
ID ABO17504 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 66
ID ADB29964 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 67
ID ADA80492 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 68
ID ADA75734 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 69
ID ADA46959 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 70
ID ADB25255 standard; protein; 312 AA.

DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 71
ID ADA93431 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 72
ID ADB26781 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 73
ID ADB31068 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 74
ID ADA60996 standard; protein; 312 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 75
ID ADB24143 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 76
ID ADA96472 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 77
ID ADA81044 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 78
ID ADA95920 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 79
ID ADB26229 standard; protein; 312 AA.
DE Human PRO polypeptide #168.

PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 80
ID ADB21714 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 81
ID ADA77493 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003086797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 82
ID ADB18233 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 83
ID ADA86916 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 84
ID ADA16524 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 85
ID ADA12953 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 86
ID ADA41821 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 87
ID ADA88019 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 88
ID ADA46407 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003054516-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 89
ID ADA17168 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 90
ID ADA42671 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 91
ID ADB28437 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 92
ID ADB28989 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 93
ID ADA76941 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 94
ID ADA88571 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 95
ID ADA97576 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 96
ID ADB27333 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US200302239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 97
ID ADB22266 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 98
ID ABO17565 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 99
ID ADA66957 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003088793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 100
ID ADB22818 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 101
ID ADB23591 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 102
ID ADA92313 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 103
ID ADB15376 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 104
ID ADB38628 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 105
ID ADB38076 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 106
ID ADB66548 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;

RESULT 107
ID ADB89628 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 108
ID ADB90360 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 109
ID ADB77590 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 110
ID ADB39461 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 111
ID ADB74726 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 112
ID ADB47084 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 113
ID ADB86691 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 114
ID ADB77296 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 115
ID ADB34453 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 116
ID ADB34210 standard; protein; 312 AA.

ID ADB35557 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 117
ID ADB33901 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 118
ID ADB35005 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 119
ID ADB36109 standard; protein; 312 AA.
DE Human PRO polypeptide SEQ ID NO 336.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 120
ID ADB46504 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 121
ID ADC28372 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 122
ID ADC39572 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 123
ID ADC40086 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 124
ID ADC18914 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 125
ID ADC34210 standard; protein; 312 AA.

DE Human secreted/transmembrane protein, #13.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 126
ID ADC29265 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 127
ID ADC28796 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 128
ID ADC40681 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 129
ID ADC19338 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054411-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 130
ID ADC33786 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 131
ID ADC12856 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 132
ID ADC50377 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 133
ID ADC71924 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 134
ID ADC59903 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 135
ID ADC52910 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 136
ID ADC57264 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 137
ID ADC60455 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 138
ID ADC50930 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 139
ID ADC65457 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 140
ID ADC54555 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 141
ID ADC53516 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 142
ID ADC59039 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 143
ID ADC55917 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087360-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 144
ID ADC58487 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein Seq ID336.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 145
ID ADC12308 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 146
ID ADC03161 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 147
ID ADC90153 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 148
ID ADC69572 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 149
ID ADC48461 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 150
ID ADD09990 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 151
ID ADD04565 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 152
ID ADC80521 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003092103-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 153
ID ADD11028 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 154
ID ADC47909 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 155
ID ADD04863 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 156
ID ADC79969 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 157
ID ADD09438 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 158
ID ADD03869 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 159
ID ADD03445 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 160
ID ADD41151 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 161
ID ADD52290 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 162
ID ADD53030 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 163
ID ADD53582 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 164
ID ADD51738 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 165
ID ADD02537 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 166
ID ADD01971 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 167
ID ADD54153 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 168
ID ADD91366 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 169
ID ADD91366 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199035-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 170
ID ADE03980 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 171
ID ADE32277 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 172
ID ADE22209 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 173
ID ADD79433 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 174
ID ADE41969 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 175
ID ADE17786 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 176
ID ADD91918 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 177
ID ADE33381 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 178
ID ADE33933 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 179
ID ADD79985 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
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RESULT 180
ID ADE93022 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 181
ID ADE19442 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 182
ID ADE34697 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 183
ID ADE18890 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 184
ID ADE43086 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 185
ID ADD95875 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 186
ID ADE22761 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 187
ID ADD78879 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 188
ID ADE32829 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 189
ID ADE42521 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 190
ID ADD80537 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 191
ID ADD89565 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 192
ID ADE40849 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 193
ID ADE04648 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 194
ID ADE92777 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 195
ID ADG21486 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 196
ID ADG23127 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 197
ID ADF97462 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 198
ID ADG80526 standard; protein; 312 AA.

DE Human PRO polypeptide #168.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 199
ID AG79974 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 200
ID ADH62536 standard; protein; 312 AA.
DE Human PRO245 protein encoded by DNA35638 CDNA.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 201
ID ADH59180 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 202
ID ADH5266 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 203
ID ADH55818 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207379-A1.
PD 08-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 204
ID ADI37959 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 205
ID ADI64986 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 206
ID ADH81899 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207388-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 207
ID ADH81347 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207377-A1.
PD 08-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 208
ID ADJ26227 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 209
ID ADM82516 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 210
ID ADN15915 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 211
ID ADN16544 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 212
ID ADN15363 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 213
ID ADN14811 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 214
ID ADI64037 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 7; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 215
ID ADI63485 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.


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RESULT 234
ID ADE91078 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #168.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 235
ID ADE95219 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 236
ID ADE93329 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 237
ID ADF34910 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 238
ID ADE98450 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 239
ID ADE92225 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 240
ID ADE90526 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 241
ID ADE91673 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 242
ID ADE98877 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 243
ID ADE91078 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #168.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 244
ID ADF73741 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 245
ID ADG2252 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 246
ID ADG22038 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 247
ID ADG20108 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 248
ID ADF98014 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 249
ID ADG24231 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 250
ID ADF98585 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 251
ID ADG03416 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207351-A1.
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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 252
ID ADF99137 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 253
ID ADG16722 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 254
ID ADG05181 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 255
ID ADG19448 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 256
ID ADF73317 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003160051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 257
ID ADG13285 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 258
ID ADG08342 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 259
ID ADG15512 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 260
ID ADF96910 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207371-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 261
ID ADG06095 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 262
ID ADG23679 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 263
ID ADG03968 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 264
ID ADG24869 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 265
ID ADG07166 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 266
ID ADG07718 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 267
ID ADG55213 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 268
ID ADG60877 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 269
ID ADG61981 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

ID ADH12583 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 289
ID ADG61429 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 290
ID ADH28516 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 291
ID ADG54661 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 292
ID ADG59701 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 293
ID ADH20376 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 294
ID ADH07231 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 295
ID ADH59776 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 296
ID ADH06804 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2004005665-A1.

PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 297
ID ADI81125 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 298
ID ADI18546 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 299
ID ADI6266 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 300
ID ADI37529 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 301
ID ADG09868 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 302
ID ADH97333 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 303
ID ADI15339 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 304
ID ADG09216 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;

Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 305
ID ADI14671 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 306
ID ADH60436 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 307
ID ADI18266 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 308
ID ADJ99493 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 309
ID ADL08686 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 310
ID ADM25031 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 311
ID ADJ63547 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 312
ID ADM29777 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 313
ID ADJ77442 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 314
ID ADJ65564 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 315
ID ADM27700 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 316
ID ADM42424 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 317
ID ADO06099 standard; protein; 312 AA.
DE Human PRO polypeptide #11.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 318
ID ADN35292 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 319
ID ADM28286 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 320
ID ADRI0951 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 321
ID ADRI7860 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.

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PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 322
ID ADI95768 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 323
ID ADI96320 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 324
ID ADI65693 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 325
ID ADT94237 standard; protein; 312 AA.
DE Human PRO245 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 326
ID ADS74499 standard; protein; 312 AA.
DE Human secreted/transmembrane protein #13.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERE/) FERARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
Query Match 100.0%; Score 1605; DB 9; Length 312;

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PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 327
ID ADS32272 standard; protein; 312 AA.
DE Novel human secreted and transmembrane protein PRO245.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 328
ID ADT03256 standard; protein; 312 AA.
DE Human PRO polypeptide #168.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 329
ID ADT03536 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 8; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 330
ID ADZ03307 standard; protein; 312 AA.
DE Human secreted/transmembrane PRO245 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 9; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 331
ID AEA37774 standard; protein; 312 AA.
DE Human secreted/transmembrane protein, #13.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1605; DB 9; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 332
ID AEB14053 standard; protein; 312 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 336.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (ISHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 100.0%; Score 1605; DB 9; Length 312;

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Best Local Similarity 100.0%; Pred. No. 5.2e-123;
RESULT 333
ID AAB50904 standard; protein; 312 AA.
DE Human PRO245 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 99.6%; Score 1599; DB 4; Length 312;
Best Local Similarity 99.7%; Pred. No. 1.6e-122;
RESULT 334
ID ADP56682 standard; protein; 323 AA.
DE Human junction adhesion molecule 2 splice variant (huJAM2sv) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 99.0%; Score 1589; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.1e-121;
RESULT 335
ID AAW85457 standard; protein; 298 AA.
DE Secreted protein encoded by clone ct864_4.
PN WO9842739-A2.
PD 01-OCT-1998.
PA (GEMY) GENETICS INST INC.
Query Match 91.9%; Score 1475; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.2e-112;
RESULT 336
ID AAU00512 standard; protein; 298 AA.
DE Human junctional adhesion protein (JAM2).
PN WO200114404-A1.
PD 01-MAR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 91.9%; Score 1475; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.2e-112;
RESULT 337
ID ABP61801 standard; protein; 298 AA.
DE Human polypeptide SEQ ID NO 155.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO) JACOBS K.
PA (MCCO) MCCOY J M.
PA (LAVA) LAVALLIE E R.
PA (COLL) COLLINS-RACIE L A.
PA (EVAN) EVANS C.
PA (MERB) MERBERG D.
PA (TREA) TREACY M.
PA (SPAU) SPAULDING V.
Query Match 91.9%; Score 1475; DB 5; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.2e-112;
RESULT 338
ID ABR58532 standard; protein; 298 AA.
DE Human vascular endothelial junction-associated molecule protein.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 91.9%; Score 1475; DB 6; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.2e-112;
RESULT 339
ID ADI47178 standard; protein; 298 AA.
DE Human JAM-3 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 91.9%; Score 1475; DB 8; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.2e-112;
RESULT 340
ID ADP56681 standard; protein; 298 AA.
DE Human junction adhesion molecule 2 (huJAM2) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 91.9%; Score 1475; DB 8; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.2e-112;
RESULT 341

ID ABM82288 standard; protein; 298 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO28687, SEQ:5880.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 91.9%; Score 1475; DB 8; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.2e-112;
RESULT 342
ID AAO16452 standard; protein; 298 AA.
DE Human junctional adhesion molecule 2 (huJAM2).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 91.7%; Score 1471; DB 6; Length 298;
Best Local Similarity 99.7%; Pred. No. 4.7e-112;
RESULT 343
ID AAW75220 standard; protein; 298 AA.
DE Human secreted protein encoded by gene 25 clone HTEEB42.
PN WO9840483-A2.
PD 17-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 91.3%; Score 1465; DB 2; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.5e-111;
RESULT 344
ID AAE26983 standard; protein; 298 AA.
DE Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
PN US2002077287-A1.
PD 20-JUN-2002.
PA (RUBE) RUBEN S M.
PA (ROSE) ROSEN C A.
PA (LIYY) LI Y.
PA (ZENG) ZENG Z.
PA (FISC) FISCHER C L.
PA (LIHH) LI H.
PA (SOPE) SOPPET D R.
PA (GENT) GENTZ R L.
PA (WEIY) WEI Y.
PA (MOOR) MOORE P A.
PA (YOUN) YOUNG P E.
PA (GREE) GREENE J M.
PA (FERR) FERRIE A M.
Query Match 91.3%; Score 1465; DB 5; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.5e-111;
RESULT 345
ID AAE27121 standard; protein; 298 AA.
DE Human gene 25 encoded secreted protein HTEEB42, SEQ ID NO:76.
PN US2002076756-A1.
PD 20-JUN-2002.
PA (RUBE) RUBEN S M.
PA (ROSE) ROSEN C A.
PA (LIYY) LI Y.
PA (ZENG) ZENG Z.
PA (KYAW) KYAW H.
PA (FISC) FISCHER C L.
PA (LIHH) LI H.
PA (SOPP) SOPPET D R.
PA (GENT) GENTZ R L.
PA (WEIY) WEI Y.
PA (MOOR) MOORE P A.
PA (YOUN) YOUNG P E.
PA (GREE) GREENE J M.
PA (FERR) FERRIE A M.
Query Match 91.3%; Score 1465; DB 5; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.5e-111;
RESULT 346
ID ABR47926 standard; protein; 298 AA.
DE Human secreted protein, SEQ ID 817.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 91.3%; Score 1465; DB 6; Length 298;
Best Local Similarity 99.3%; Pred. No. 1.5e-111;

RESULT 347
ID ABR00172 standard; protein; 298 AA.
DE Human gene 162 encoded secreted protein HTSEB42, SEQ ID NO:461.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 91.3%; Score 1465; DB 6; Length 298;
Pred. No. 1.5e-111;
RESULT 348
ID ABU64994 standard; protein; 298 AA.
DE Human secreted protein gene 25, protein.
PN US2002172994-A1.
PD 21-NOV-2002.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENTZ) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
Query Match
Best Local Similarity 91.3%; Score 1465; DB 6; Length 298;
Pred. No. 1.5e-111;
RESULT 349
ID ADB91670 standard; protein; 298 AA.
DE Human secreted protein #SEQ ID 616.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 91.3%; Score 1465; DB 7; Length 298;
Pred. No. 1.5e-111;
RESULT 350
ID ADC74331 standard; protein; 298 AA.
DE Human secreted protein - SEQ ID 964.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 91.3%; Score 1465; DB 7; Length 298;
Pred. No. 1.5e-111;
RESULT 351
ID ADG89803 standard; protein; 298 AA.
DE Human protein from secreted protein gene 25.
PN US2003225009-A1.
PD 04-DEC-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENTZ) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
Query Match
Best Local Similarity 91.3%; Score 1465; DB 8; Length 298;
Pred. No. 1.5e-111;
RESULT 352
ID AAM23693 standard; protein; 303 AA.
DE Human EST encoded protein SEQ ID NO: 1218.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.

Query Match
Best Local Similarity 90.9%; Score 1459.5; DB 4; Length 303;
Pred. No. 4.2e-111;
RESULT 353
ID ABG22341 standard; protein; 388 AA.
DE Novel human diagnostic protein #22332.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 74.7%; Score 1199.5; DB 4; Length 388;
Pred. No. 1.2e-89;
RESULT 354
ID AAO30179 standard; protein; 235 AA.
DE Human novel splice variant of VEJAM (NOJAM).
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GEST) GENSET SA.
Query Match
Best Local Similarity 74.6%; Score 1197; DB 6; Length 235;
Pred. No. 9.9e-90;
RESULT 355
ID AAB27273 standard; protein; 298 AA.
DE Human confluency regulated adhesion molecule 2 #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 71.3%; Score 1144; DB 3; Length 298;
Pred. No. 3e-85;
RESULT 356
ID AAB27275 standard; protein; 298 AA.
DE Murine confluency regulated adhesion molecule 2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 71.3%; Score 1144; DB 3; Length 298;
Pred. No. 3e-85;
RESULT 357
ID AAM41947 standard; protein; 222 AA.
DE Human polypeptide SEQ ID NO 6878.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 67.9%; Score 1090; DB 4; Length 222;
Pred. No. 5.4e-81;
RESULT 358
ID AAB70500 standard; protein; 215 AA.
DE Angiogenesis protein AAL protein sequence (Fig 8).
PN WO20011086-A2.
PD 15-FEB-2001.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 65.6%; Score 1053; DB 4; Length 215;
Pred. No. 5.6e-78;
RESULT 359
ID AAB27277 standard; protein; 213 AA.
DE Human confluency regulated adhesion molecule 2 #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity 64.7%; Score 1039; DB 3; Length 213;
Pred. No. 7.8e-77;
RESULT 360
ID ABG22338 standard; protein; 140 AA.
DE Novel human diagnostic protein #22329.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 40.5%; Score 649.5; DB 4; Length 140;
Pred. No. 3.8e-45;
RESULT 361
ID AAM40161 standard; protein; 107 AA.
DE Human polypeptide SEQ ID NO 3306.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 30.8%; Score 494; DB 4; Length 107;
Pred. No. 3.8e-45;

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Best Local Similarity 100.0%; Pred. No. 1.5e-32;
RESULT 362
ID AAB27278 standard; protein; 310 AA.
DE Murine confluency regulated adhesion molecule 1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMP DICTAGENE SA.
Query Match 29.8%; Score 478; DB 3; Length 310;
Best Local Similarity 36.3%; Pred. No. 1.2e-30;
RESULT 363
ID AAB27272 standard; protein; 310 AA.
DE Human confluency regulated adhesion molecule 1 #1.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMP DICTAGENE SA.
Query Match 29.8%; Score 478; DB 3; Length 310;
Best Local Similarity 36.3%; Pred. No. 1.2e-30;
RESULT 364
ID ADP69027 standard; protein; 310 AA.
DE Human NOV2b protein SEQ ID NO:22.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 29.1%; Score 466.5; DB 8; Length 310;
Best Local Similarity 37.4%; Pred. No. 1.1e-29;
RESULT 365
ID ADP69025 standard; protein; 310 AA.
DE Human NOV2a protein SEQ ID NO:20.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 29.0%; Score 465.5; DB 8; Length 310;
Best Local Similarity 37.4%; Pred. No. 1.3e-29;
RESULT 366
ID ADP69035 standard; protein; 310 AA.
DE Human NOV2f protein SEQ ID NO:30.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 28.8%; Score 462.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.2e-29;
RESULT 367
ID AAY96735 standard; protein; 310 AA.
DE PRO1868, an A33 antigen homologue.
PN WO200036102-A2.
PD 22-JUN-2000.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 3; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 368
ID AAB33457 standard; protein; 310 AA.
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 3; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 369
ID AAB27276 standard; protein; 310 AA.
DE Human confluency regulated adhesion molecule 1 #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMP DICTAGENE SA.
Query Match 28.8%; Score 461.5; DB 3; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 370
ID AAB80272 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;

Best Local Similarity 100.0%; Pred. No. 1.5e-32;
RESULT 371
ID AAM93905 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 4051.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 372
ID AAM93323 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 2845.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 373
ID AAU12440 standard; protein; 310 AA.
DE Human PRO1868 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 374
ID AAB80383 standard; protein; 310 AA.
DE Secreted protein encoded by gene #13.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 375
ID AAB80408 standard; protein; 310 AA.
DE Secreted protein encoded by gene #38.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 376
ID AAB80409 standard; protein; 310 AA.
DE Secreted protein encoded by gene #39.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 4; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 377
ID ABG92709 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2002098506-A1.
PD 25-JUL-2002.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 378
ID ABG91361 standard; protein; 310 AA.
DE Novel human secreted protein #7.
PN US2002098505-A1.
PD 25-JUL-2002.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 379
ID ABB84947 standard; protein; 310 AA.
DE Human PRO1868 protein sequence SEQ ID NO:262.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 380
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ID ABG65297 standard; protein; 310 AA.
DE Human albumin fusion protein #1972.
PD WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 381
ID ABG65296 standard; protein; 310 AA.
DE Human albumin fusion protein #1971.
PD WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 382
ID ABG65298 standard; protein; 310 AA.
DE Human albumin fusion protein #1973.
PD WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 383
ID ARG31401 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.
PD US2002098507-A1.
PD 25-JUL-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 384
ID ABB95553 standard; protein; 310 AA.
DE Human angiogenesis related protein PRO1868 SEQ ID NO: 262.
PD WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 5; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 385
ID ABU71650 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PD US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 386
ID ABU72377 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PD US2002182618-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 387
ID ABU80867 standard; protein; 310 AA.
DE Human secreted and transmembrane polypeptide PRO1868.

PN US2002192668-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 388
ID ABO17884 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PD US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 389
ID ABU71505 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PD US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 390
ID ADA57610 standard; protein; 310 AA.
DE Human secreted protein #592.
PD WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 391
ID ADA57611 standard; protein; 310 AA.
DE Human secreted protein #592.
PD WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 392
ID ADA57309 standard; protein; 310 AA.
DE Human secreted protein #592.
PD WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 393
ID ABP71277 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (JAM3).
PD WO2003006673-A2.
PD 23-JAN-2003.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 394
ID ARU81138 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PD US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 395
ID ABU71951 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PD US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 396
ID ABO01834 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PD US2002197671-A1.

Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 415
ID ADA61761 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 416
ID ADB19546 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 417
ID ADB28087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 418
ID ADA86566 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 419
ID ADB16130 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 420
ID ADA47916 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 421
ID ADA18484 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 422
ID ABO32816 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 423
ID ADA67711 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;

Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 424
ID ADB30718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 425
ID ADA86014 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 426
ID ADA97226 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 427
ID ADA79530 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 428
ID ADA87669 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 429
ID ADB16871 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 430
ID ABO34876 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 431
ID ADA16459 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 432
ID ADA91963 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;

RESULT 433
ID ADB15026 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 434
ID ADB18987 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 435
ID ADA94202 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 436
ID ADB20098 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 437
ID ADB13410 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 438
ID ABO43417 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 439
ID ADA74664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 440
ID ADA42604 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 441
ID ADB24897 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 442
ID ADB25457 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 443
ID ADA75384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 444
ID ADA85462 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 445
ID ADA84910 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 446
ID ABO17554 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 447
ID ADB30166 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 448
ID ADA80694 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 449
ID ADA75936 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 450
ID ADA47161 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 6; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 451
ID ADB25457 standard; protein; 310 AA.

DE Human PRO polypeptide SEQ ID NO 538.
 PN US2003077715-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 452
 ID ADA93633 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003077721-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 453
 ID ADB26983 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003092147-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 454
 ID ADB31270 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003096386-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 455
 ID ABU62957 standard; protein; 310 AA.
 DE Human PRO1868 protein.
 PN US2003054447-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 456
 ID ADA61198 standard; protein; 310 AA.
 DE Homo sapiens.
 PN US2003049817-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 457
 ID ADB24345 standard; protein; 310 AA.
 DE Human PRO polypeptide SEQ ID NO 538.
 PN US2003077714-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 458
 ID ADA96674 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003082690-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 459
 ID ADA81246 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003082702-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 460
 ID ADA96122 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.

PN US2003082759-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 461
 ID ADB26431 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003082760-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 462
 ID ADB21916 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082765-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 6; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 463
 ID ADA77695 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003068797-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 464
 ID ADB18435 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003077710-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 465
 ID ADA87118 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082709-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 466
 ID ADA16883 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003039969-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 467
 ID ADA13312 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003049622-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 468
 ID ADA42180 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003082540-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 7; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 469
 ID ADA88221 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003082700-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 470
ID ADA46609 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 471
ID ADA17527 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 472
ID ADA43030 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 473
ID ADB28639 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 474
ID ADB29191 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 475
ID ABO01894 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003027256-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 476
ID ADA77143 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 477
ID ADA88773 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 478
ID ADA97778 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082686-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 479
ID ADB27535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 480
ID ADB22468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 481
ID ABO17615 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003084923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 482
ID ADA67159 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 483
ID ADB23020 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 484
ID ADB23793 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 485
ID ADA92515 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 486
ID ADB15578 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 487
ID ADB38830 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 488
ID ADB38830 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;

RESULT 488
ID ADB38278 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082696-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 489
ID ADB66750 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 490
ID ADB89830 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 491
ID ADB90562 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 492
ID ADB77948 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 493
ID ADB39663 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 494
ID ADB75084 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 495
ID ADB47286 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 496
ID ADB86993 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 497
ID ADB77498 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 498
ID ADB34655 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 499
ID ADB35759 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 500
ID ADB34103 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 501
ID ADB35207 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 502
ID ADB36311 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 503
ID ADB46706 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 504
ID ADC28731 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 505
ID ADC39931 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 506
ID ADC40445 standard; protein; 310 AA.

DE Human secreted/transmembrane protein, #65.
PN US2003059829-A1.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 507
ID ADC19269 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 508
ID ADC34569 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 509
ID ADC29624 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 510
ID ADC29155 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 511
ID ADC41040 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 512
ID ADC19697 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 513
ID ADC34145 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 514
ID ADC13215 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 515
ID RAE38826 standard; protein; 310 AA.
DE Human PRO1868 protein.

PN US2003077657-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 516
ID ADC50579 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 517
ID ADC72126 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 518
ID ADC60105 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 519
ID ADC53112 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 520
ID ADC57466 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 521
ID ADC60657 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 522
ID ADC51132 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 523
ID ADC65659 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 524
ID ADC54757 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087363-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 525
ID ADC53718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 526
ID ADC59241 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 527
ID ADC56119 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 528
ID ADC58689 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 529
ID ADC12667 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 530
ID ADC74383 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1016.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 531
ID ADC74606 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1239.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 532
ID ADC74607 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1240.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 533
ID ADD03363 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092104-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 534
ID ADC90355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 535
ID ADC69774 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 536
ID ADC48663 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 537
ID ADD10192 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 538
ID ADD04767 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 539
ID ADC80723 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 540
ID ADD11230 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 541
ID ADD10551 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 542
ID ADC48111 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

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Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 543
ID ADD05222 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 544
ID ADC80171 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 545
ID ADD11511 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 546
ID ADD09640 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 547
ID ADD04228 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 548
ID ADD03804 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 549
ID ADD41353 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 550
ID ADD52492 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 551
ID ADD53232 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 552
ID ADD53784 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 553
ID ADD37304 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 554
ID ADD51940 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 555
ID ADD02739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 556
ID ADD38106 standard; protein; 310 AA.
DE Human secreted protein #289.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 557
ID ADD38009 standard; protein; 310 AA.
DE Human secreted protein #192.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 558
ID ADD38105 standard; protein; 310 AA.
DE Human secreted protein #288.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 559
ID ADD02173 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 560
ID ADD54355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
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DE Human PRO polypeptide #269.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 580
ID ADG79081 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 581
ID ADE33031 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 582
ID ADE42723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 583
ID ADH80739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 584
ID ADD89767 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 585
ID ADE41051 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 586
ID ADE04850 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 587
ID ADE92979 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 588
ID ADG21688 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.

PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 589
ID ADG23329 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 590
ID ADF97664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 591
ID ADG80728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 592
ID ADG80176 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 593
ID ADH62558 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 594
ID ADH59539 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 595
ID ADH55468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 596
ID ADH56020 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 597
ID ADI39318 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 598
ID ADI64239 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 599
ID ADI65188 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 600
ID ADI63687 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 601
ID ADH82101 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 602
ID ADH81549 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 603
ID ADJ58518 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003170864-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 604
ID ADJ26586 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 605
ID ADM82718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;

Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 606
ID ADN16117 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 607
ID ADN16746 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 608
ID ADN15565 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 609
ID ADN15013 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 7; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 610
ID ADC81275 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 611
ID ADE79501 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 612
ID ADD76723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 613
ID ADD88087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 614
ID ADD86491 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;

RESULT 615
ID ADE79925 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 616
ID ADE75939 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 617
ID ADE73601 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 618
ID ADE41512 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 619
ID ADE23515 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 620
ID ADE24067 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 621
ID ADE24710 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 622
ID ADD87535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 623
ID ADE89401 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 624
ID ADE98809 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 625
ID ADE18540 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 626
ID ADE88849 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 627
ID ADE99690 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 628
ID ADE94869 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 629
ID ADE91280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 630
ID ADE95421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 631
ID ADE93531 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 632
ID ADF35112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 633
ID ADE98809 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 634
ID ADE98809 standard; protein; 310 AA.

DE Human secreted/transmembrane protein, #65.
 PN US2003211569-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 634
 ID ADE92427 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003199051-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 635
 ID ADE90728 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003199063-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 636
 ID ADE91875 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003199058-A1.
 PD 23-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 637
 ID ADE99236 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003211568-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 638
 ID ADG40706 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003225253-A1.
 PD 04-DEC-2003.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A. J.
 PA (GODO/) GODOWSKI P. J.
 PA (GURN/) GURNEY A. L.
 PA (MATH/) MATHER J. P.
 PA (WILL/) WILLIAMS P. M.
 PA (WOOD/) WOOD W. I.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 639
 ID ADF74100 standard; protein; 310 AA.
 DE Human secreted/transmembrane protein, #65.
 PN US2003180312-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 640
 ID ADG02454 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207352-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 641
 ID ADG22240 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003207360-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 642
 ID ADG20310 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207376-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 643
 ID ADF98216 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207422-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 644
 ID ADG24433 standard; protein; 310 AA.
 DE Novel human secreted and transmembrane protein PRO1868.
 PN US2003207426-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 645
 ID ADF98787 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003208055-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 646
 ID ADG03618 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207351-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 647
 ID ADF99339 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207353-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 648
 ID ADG16924 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207359-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 649
 ID ADG05383 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207375-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 28.8%; Score 461.5; DB 8; Length 310;
 Best Local Similarity 37.1%; Pred. No. 2.7e-29;
 RESULT 650
 ID ADG19650 standard; protein; 310 AA.
 DE Human PRO polypeptide #269.
 PN US2003207425-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.

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Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 651
ID ADF73676 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 652
ID ADG13487 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 653
ID ADG09544 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 654
ID ADG15714 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 655
ID ADF97112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 656
ID ADG06297 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 657
ID ADG23381 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 658
ID ADG04170 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 659
ID ADG25071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 660
ID ADG07368 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 661
ID ADG07920 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 662
ID ADG55415 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 663
ID ADG61079 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 664
ID ADG62183 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 665
ID ADG92519 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 666
ID ADG82384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 667
ID ADG57623 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 668
ID ADG57071 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
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RESULT 669
ID ADG55967 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 670
ID ADG58727 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 671
ID ADG71093 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 672
ID ADG92946 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 673
ID ADG58175 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 674
ID ADG53759 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 675
ID ADG71645 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 676
ID ADG81832 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 677
ID ADH30794 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 678
ID ADH12161 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 679
ID ADG52583 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 680
ID ADG54311 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 681
ID ADG81280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 682
ID ADG56519 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 683
ID ADH12785 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 684
ID ADG61631 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 685
ID ADH28718 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 686
ID ADG54863 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 687
ID ADG59903 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.

PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 688
ID ADH20735 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 689
ID ADH43695 standard; protein; 310 AA.
DE Human PRO polypeptide #131.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 690
ID ADH07590 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 691
ID ADH60135 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 692
ID ADH07163 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 693
ID ADI81327 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 694
ID ADI18905 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;

RESULT 695
ID ADI65625 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 696
ID ADI37884 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 697
ID ADG10070 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 698
ID ADH97684 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 699
ID ADI15541 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 700
ID ADG09418 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 701
ID ADI66052 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 702
ID ADI10341 standard; protein; 310 AA.
DE Human PRO1868 protein from DNA77624-2515 clone.
PN US2003228664-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 703
ID ADI14873 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 704
ID ADI14873 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;

ID ADH60795 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 705
ID ADI18468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 706
ID ADJ9852 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 707
ID ADI09045 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 708
ID ADI47177 standard; protein; 310 AA.
DE Human JAM-2 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 709
ID ADM25386 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 710
ID ADJ63749 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004039164-A1.
PD 28-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 711
ID ADM30136 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 712
ID ADL78563 standard; protein; 310 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2045.
PN US2004010134-A1.

PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 713
ID ADL78564 standard; protein; 310 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2046.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 714
ID ADL78565 standard; protein; 310 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2047.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 715
ID ADJ77644 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 716
ID ADK83040 standard; protein; 310 AA.
DE Human PRO polypeptide #131.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 717
ID ADJ65766 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 718
ID ADL30812 standard; protein; 310 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2845.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 719
ID ADL32018 standard; protein; 310 AA.
DE Human protein encoded by a full length cDNA clone SeqID 4051.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 720
ID ADM27902 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 721
ID ADM42626 standard; protein; 310 AA.

DE Human PRO polypeptide #269.
PN US2004059424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 722
ID AD006458 standard; protein; 310 AA.
DE Human PRO polypeptide #60.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 723
ID ADN35310 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 724
ID ADM28488 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 725
ID ADP69033 standard; protein; 310 AA.
DE Human NOV2e protein SEQ ID NO:28.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 726
ID ADR13130 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 727
ID ADR18219 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANG/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 731
ID ADS32474 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 732
ID ADT03458 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 733
ID ADT03895 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.

PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 728
ID ADI95970 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 729
ID ADI96522 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 730
ID ADS74858 standard; protein; 310 AA.
DE Human secreted/transmembrane protein #65.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANG/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 731
ID ADS32474 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 732
ID ADT03458 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 733
ID ADT03895 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.

Query Match 28.8%; Score 461.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 734
ID ABO3509 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO1868 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 9; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 735
ID ABA38133 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 28.8%; Score 461.5; DB 9; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 736
ID ABB14255 standard; protein; 310 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 538.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE) BAKER K P.
PA (BERE) BRESINI M.
PA (DEFO) DEFORGE L.
PA (DESN) DESNOYERS L.
PA (FILV) FILVAROFF E.
PA (GAOW) GAO W.
PA (GERE) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (SHER) SHERWOOD S.
PA (SMIT) SMITH V.
PA (STEW) STEWART T A.
PA (TUMA) TUMAS D.
PA (WATA) WATANABE C K.
PA (WOOD) WOOD W I.
PA (ZHAN) ZHANG Z.
Query Match 28.8%; Score 461.5; DB 9; Length 310;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 737
ID AAB38383 standard; protein; 311 AA.
DE Human secreted protein encoded by gene 13 clone HAPSA79.
PN WO2000061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 3; Length 311;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 738
ID AAB38384 standard; protein; 311 AA.
DE Human secreted protein encoded by gene 13 clone HAPSA79.
PN WO2000061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 3; Length 311;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 739
ID AAB38333 standard; protein; 311 AA.
DE Human secreted protein encoded by gene 13 clone HAPSA79.
PN WO2000061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 3; Length 311;
Best Local Similarity 37.1%; Pred. No. 2.7e-29;
RESULT 740
ID AAB80431 standard; peptide; 339 AA.
DE Gene #13 associated peptide #1.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.8%; Score 461.5; DB 4; Length 339;

Best Local Similarity 37.1%; Pred. No. 3e-29;
RESULT 741
ID ABP41902 standard; protein; 329 AA.
DE Human ovarian antigen HISAFA60, SEQ ID NO:3034.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.7%; Score 460.5; DB 5; Length 329;
Best Local Similarity 37.9%; Pred. No. 3.5e-29;
RESULT 742
ID AAO18453 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (huJAM3).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 28.6%; Score 459.5; DB 6; Length 310;
Best Local Similarity 37.0%; Pred. No. 3.9e-29;
RESULT 743
ID AAY96294 standard; protein; 310 AA.
DE Human IGFAM-6 immunoglobulin.
PN WO200029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 28.4%; Score 456.5; DB 3; Length 310;
Best Local Similarity 37.1%; Pred. No. 7e-29;
RESULT 744
ID ADP56683 standard; protein; 310 AA.
DE Human junction adhesion molecule 3 (huJAM3) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 28.4%; Score 456.5; DB 8; Length 310;
Best Local Similarity 37.1%; Pred. No. 7e-29;
RESULT 745
ID AAB39254 standard; protein; 285 AA.
DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:134.
PN WO2000056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 28.3%; Score 455; DB 3; Length 285;
Best Local Similarity 39.7%; Pred. No. 8.3e-29;
RESULT 746
ID AAO30255 standard; protein; 87 AA.
DE Human novel splice variant of VEJAM (NoJAM) fragment.
PN WO2003046180-A2.
PD 05-JUN-2003.
PA (GEST) GENSET SA.
Query Match 27.9%; Score 448; DB 6; Length 87;
Best Local Similarity 98.8%; Pred. No. 6.8e-29;
RESULT 747
ID ABB06037 standard; protein; 321 AA.
DE Human NS protein sequence SEQ ID NO:129.
PN WO200206315-A2.
PD 24-JAN-2002.
PA (COMP-) COMPUGEN LTD.
Query Match 27.7%; Score 444; DB 5; Length 321;
Best Local Similarity 35.8%; Pred. No. 7.7e-28;
RESULT 748
ID ADP29461 standard; protein; 90 AA.
DE Human secreted protein SEQ ID #228.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 27.4%; Score 439; DB 8; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.9e-28;
RESULT 749
ID AAU17996 standard; protein; 301 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 141.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.5%; Score 409; DB 4; Length 301;
Best Local Similarity 34.3%; Pred. No. 5.2e-25;

RESULT 750
ID ABB10232 standard; protein; 301 AA.
DE Human cDNA SEQ ID NO: 540.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.5%; Score 409; DB 4; Length 301;
Best Local Similarity 34.3%; Pred. No. 5.2e-25;
RESULT 751
ID ABP66819 standard; protein; 301 AA.
DE Human polypeptide SEQ ID NO 540.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 25.5%; Score 409; DB 5; Length 301;
Best Local Similarity 34.3%; Pred. No. 5.2e-25;
RESULT 752
ID ADB31620 standard; protein; 301 AA.
DE Human novel protein SEQ ID NO 141.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.5%; Score 409; DB 7; Length 301;
Best Local Similarity 34.3%; Pred. No. 5.2e-25;
RESULT 753
ID ADR41522 standard; protein; 318 AA.
DE Human CD-like molecule HRACI03, SEQ ID NO:321.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.5%; Score 409; DB 5; Length 318;
Best Local Similarity 34.3%; Pred. No. 5.6e-25;
RESULT 754
ID ADJ67617 standard; protein; 351 AA.
DE Human ovarian specific polypeptide SEQ ID NO:331.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 25.5%; Score 408.5; DB 8; Length 351;
Best Local Similarity 35.1%; Pred. No. 7e-25;
RESULT 755
ID AAY23321 standard; protein; 299 AA.
DE Amino acid sequence of the PRO301 polypeptide.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH-) GENENTECH INC.
Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 756
ID AAW74464 standard; protein; 299 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 757
ID AAY08071 standard; protein; 299 AA.
DE Human PRO307 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 758
ID AAY13364 standard; protein; 299 AA.
DE Amino acid sequence of protein PRO301.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 759
ID AAY76011 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:189.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 760
ID AAY76076 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:331.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 761
ID AAY70670 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 762
ID AAB24405 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:90.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 763
ID AAY95344 standard; protein; 299 AA.
DE Human PRO301 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 764
ID ADC78439 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 25.2%; Score 404; DB 3; Length 299;
Best Local Similarity 35.9%; Pred. No. 1.3e-24;
RESULT 765
ID AAB80232 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 766
ID AAM93577 standard; protein; 299 AA.
DE Human polypeptide, SEQ ID NO: 3365.
PN EPL130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 767
ID AAB56015 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 331.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;

RESULT 768
ID AAB55950 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 189.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 769
ID AAB31202 standard; protein; 299 AA.
DE Amino acid sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 770
ID AAU00823 standard; protein; 299 AA.
DE Human immune response protein PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 771
ID AAU12354 standard; protein; 299 AA.
DE Human PRO301 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 772
ID AAB53086 standard; protein; 299 AA.
DE Human angiogenesis-associated protein PRO301, SEQ ID NO:119.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 773
ID AAU14405 standard; protein; 299 AA.
DE Human novel protein #276.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 774
ID AAU14404 standard; protein; 299 AA.
DE Human novel protein #275.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 775
ID AAU14168 standard; protein; 299 AA.
DE Human novel protein #39.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 776
ID AAB03896 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein fragment, SEQ ID NO:148.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 777
ID AAE03840 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO: 86.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 778
ID AAE03870 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO:116.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 4; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 779
ID ABB90290 standard; protein; 299 AA.
DE Human polypeptide SEQ ID NO 2666.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 780
ID ABB84843 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:54.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 781
ID ABG64551 standard; protein; 299 AA.
DE Human albumin fusion protein #1226.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 782
ID ABG64552 standard; protein; 299 AA.
DE Human albumin fusion protein #1227.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 783
ID ABB72215 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 331.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 784
ID ABB72150 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 189.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 25.2%; Score 404; DB 5; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 785
ID ABB95449 standard; protein; 299 AA.
DE Human angiogenesis related protein PRO301 SEQ ID NO: 54.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.

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PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match 25.2%; Score 404; DB 5; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 786
ID ABU71610 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 787
ID ABO17798 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 788
ID ABU71465 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 789
ID ABO25173 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 790
ID ABU81052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 791
ID ABU71911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 792
ID ABO01794 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 793
ID ABU66752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003036180-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 794
ID ABU54367 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 795
ID ABU67291 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 796
ID ABO47382 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 797
ID ABU59833 standard; protein; 299 AA.
DE Novel secreted and transmembrane protein PRO301.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 798
ID ABO25023 standard; protein; 299 AA.
DE Human secreted/transmembrane protein (PRO) #183.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 799
ID ABU64519 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #23.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 800
ID ABU72059 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 801
ID ABU67365 standard; protein; 299 AA.
DE Human secreted protein PRO301.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 802
ID ABU67160 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032062-A1.
PD 13-FEB-2003.

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PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 803
ID ABO14885 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 804
ID ABO07736 standard; protein; 299 AA.
DE Human A-33 related antigen PRO301.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 805
ID AAO16451 standard; protein; 299 AA.
DE Human junctional adhesion molecule 1 (hwJAM1).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 806
ID ABU67028 standard; protein; 299 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 366.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 807
ID ABU69642 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 808
ID ABU79802 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 809
ID ABO14824 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 810
ID ADA45985 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 811
ID ADA76316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 812
ID ADB29324 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 813
ID ADA18966 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 814
ID ADA61589 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 815
ID ADB19374 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 816
ID ADB27915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 817
ID ADA86394 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 818
ID ADB15958 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 819
ID ADA47744 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 820
ID ADA18180 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 821
ID ADA76316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

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Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 821
ID ABO32776 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 822
ID ADA67539 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 823
ID ADB30546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 824
ID ADA85842 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 825
ID ADA97054 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 826
ID ADA79358 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 827
ID ADA87497 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 828
ID ADB16699 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 829
ID ABO34836 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 830
ID ADA16155 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 831
ID ADA91791 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 832
ID ADB14854 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 833
ID ADA47263 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 834
ID ADB18815 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 835
ID ADA94030 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 836
ID ADB19926 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 837
ID ADB13238 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 838
ID ABO43331 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 839
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ID ADA74492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 840
ID ADA42300 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 841
ID ADB24725 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 842
ID ADA82249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 843
ID ADA75212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 844
ID ADA85290 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 845
ID ADA84738 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 846
ID ABO17514 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 847
ID ADB29994 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 848
ID ADA80522 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 849
ID ADA75764 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 850
ID ADA46989 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 851
ID ADB25285 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 852
ID ADA93461 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 853
ID ADB26811 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 854
ID ADB31098 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 855
ID ADA61026 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 856
ID ADB24173 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 6; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 857
ID ADA96502 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

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PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 858
ID ADA81074 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 859
ID ADA95950 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 860
ID ADB26259 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 861
ID ADB21744 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 6; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 862
ID ADA77523 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 863
ID ADB18263 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 864
ID ADA86946 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 865
ID ADA16579 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 866
ID ADA13008 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049622-A1.

PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 867
ID ADA41876 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 868
ID ADA88049 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 869
ID ADA46437 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 870
ID ADA17223 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 871
ID ADA42726 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 872
ID ADB28467 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 873
ID ADB29019 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 874
ID ADA76971 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 25.2%; Score 404; DB 7; Length 299;
  Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 875
ID ADA88601 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073213-A1.
PD 17-APR-2003.
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PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 876
ID ADA97606 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 877
ID ADB27363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 878
ID ADB22296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 879
ID ABO19860 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO302.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 880
ID ABO17575 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 881
ID ADA65987 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 882
ID ADB22848 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 883
ID ADB23621 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 884
ID ADA92343 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 885
ID ADB15406 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 886
ID ADB38658 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 887
ID ADB38106 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 888
ID ADB66578 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 889
ID ADB89658 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 890
ID ADB90390 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 891
ID ADB77645 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 892
ID ADB39491 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 893
ID ADB74781 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 894
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ID ADB47114 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 895
ID ADB86721 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 896
ID ADB77326 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 897
ID ADB34483 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 898
ID ADB35587 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 899
ID ADB33931 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 900
ID ADB35035 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 901
ID ADB36139 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
FN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 902
ID ADB46534 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 903
ID ADB33841 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 904
ID ADC39627 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 905
ID ADC40141 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 906
ID ADC18969 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 907
ID ADC34265 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 908
ID ADC29320 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 909
ID ADC28851 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 910
ID ADC40736 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 911
ID ADC19393 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 912
ID ADC33841 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.

PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 913
ID ADC12911 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein, #25.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 914
ID ADC50407 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 915
ID ADC71954 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 916
ID ADC59933 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 917
ID ADC52940 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 918
ID ADC57294 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 919
ID ADC60485 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 920
ID ADC50960 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 921
ID ADC65487 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087362-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 922
ID ADC54585 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 923
ID ADC53546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 924
ID ADC59069 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 925
ID ADC55947 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 926
ID ADC58517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 927
ID ADC12363 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 928
ID ADD03191 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 929
ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 930
ID ADC69602 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194770-A1.
PD 16-OCT-2003.

Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 949
ID ADD51768 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 950
ID ADD02567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 951
ID ADD02001 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 952
ID ADD54183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 953
ID ADD92500 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 954
ID ADD91396 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 955
ID ADE04010 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 956
ID ADE32307 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 957
ID ADE22239 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 958
ID ADD79463 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 959
ID ADE41999 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 960
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 961
ID ADD91948 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 962
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 963
ID ADE33963 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 964
ID ADD80015 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 965
ID ADD93052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 966
ID ADE19472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 967
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;

ID ADE34752 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 968
ID ADE18920 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 969
ID ADE43116 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 970
ID ADE95905 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 971
ID ADE22791 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 972
ID ADD78909 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 973
ID ADE32859 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 974
ID ADE42551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 975
ID ADD80567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 976
ID ADD89595 standard; protein; 299 AA.

DE Human PRO polypeptide #183.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 977
ID ADE40879 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 978
ID ADE04678 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 979
ID ADE92807 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 980
ID ADG21516 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 981
ID ADG23157 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 982
ID ADF97492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 983
ID ADG80556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 984
ID ADG80004 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 7; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 985
ID ADG63772 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.

PN US2003170721-A1.
 PD 11-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 986
 ID ADH62528 standard; protein; 299 AA.
 DE Human PRO301 protein.
 PN US2003171568-A1.
 PD 11-SEP-2003.
 PA (ASHK/) ASHKENAZI A.
 PA (FONG/) FONG S.
 PA (GODD/) GODDARD A.
 PA (GURN/) GURNEY A L.
 PA (NAPI/) NAPIER M A.
 PA (TUMA/) TUMAS D.
 PA (WOOD/) WOOD W I.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 987
 ID ADH59235 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003039972-A1.
 PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 988
 ID ADH5296 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207381-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 989
 ID ADH55848 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207379-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 990
 ID ADI38014 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003054352-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 991
 ID ADI64067 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207385-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 992
 ID ADI65016 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207386-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 993
 ID ADI63515 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207387-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.

Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 994
 ID ADH81929 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207388-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 995
 ID ADH81377 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003207377-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 996
 ID ADJ26282 standard; protein; 299 AA.
 DE Human secreted/transmembrane protein, #25.
 PN US2003054349-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 997
 ID ADM82546 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003087355-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 998
 ID ADN15945 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003087353-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 999
 ID ADN16574 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003087385-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 1000
 ID ADN15393 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003087356-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 1001
 ID ADN14841 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003087357-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 7; Length 299;
 Best Local Similarity 35.2%; Pred. No. 1.3e-24;
 RESULT 1002
 ID ADC81103 standard; protein; 299 AA.
 DE Novel human secreted and transmembrane protein PRO301.
 PN US2003092115-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 25.2%; Score 404; DB 8; Length 299;

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Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1003
ID ADE79197 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1004
ID ADD76551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1005
ID ADD87915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1006
ID ADD86319 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1007
ID ADE79621 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1008
ID ADE75767 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1009
ID ADE73297 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1010
ID ADE41304 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1011
ID ADE23343 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1012
ID ADE23895 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1013
ID ADE24538 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1014
ID ADD87363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1015
ID ADE89229 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1016
ID ADE41186 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1017
ID ADE73832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1018
ID ADE18368 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1019
ID ADE88677 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1020
ID ADE99386 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1021
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ID ADE94697 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1022
ID ADE91108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1023
ID ADE95249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1024
ID ADE93359 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1025
ID ADF34940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1026
ID ADE98505 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1027
ID ADE92255 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1028
ID ADE90556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1029
ID ADE91703 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1030
ID ADE98932 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1031
ID ADG40402 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1032
ID ADF73796 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1033
ID ADG02282 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1034
ID ADG22068 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1035
ID ADG20138 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1036
ID ADF98044 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1037
ID ADG24261 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1038
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003208055-A1.
PD 06-NOV-2003.

Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1057
ID ADG62011 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1058
ID ADG92215 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1059
ID ADG82212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1060
ID ADG57451 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1061
ID ADG6899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1062
ID ADG55795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1063
ID ADG5855 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1064
ID ADG70921 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1065
ID ADG92642 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;

RESULT 1066
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1067
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1068
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1069
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1070
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1071
ID ADG63621 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1072
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1073
ID ADG52411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1074
ID ADG54139 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1075
ID ADG81108 standard; protein; 299 AA.

DE Human PRO polypeptide #183.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1076
ID ADG56347 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1077
ID ADH12613 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1078
ID ADG61459 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1079
ID ADH28546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1080
ID ADG54691 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1081
ID ADG59731 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1082
ID ADH20431 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1083
ID ADH43487 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1084
ID ADH07286 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US200400548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1085
ID ADH59831 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1086
ID ADH06859 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1087
ID ADI18155 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1088
ID ADI18601 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1089
ID ADI65321 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1090
ID ADI37584 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1091
ID ADG09898 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;

RESULT 1092
ID ADH97380 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1093
ID ADI15369 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1094
ID ADG09246 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1095
ID ADI65748 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1096
ID ADI14701 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1097
ID ADH60491 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1098
ID ADI18296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1099
ID ADJ99548 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1100
ID ADI08741 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.

PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1101
ID ADI47176 standard; protein; 299 AA.
DE Human JAM-1 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1102
ID ADM25082 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1103
ID ADK40844 standard; protein; 299 AA.
DE Human platelet FII receptor #1.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UINY) UNIV NEW YORK STATE RES FOUND.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1104
ID ADJ63577 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1105
ID ADM29832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1106
ID ADL77818 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1107
ID ADL77819 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1301.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1108
ID ADJ77472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1109
ID ADK82832 standard; protein; 299 AA.

DE Human PRO polypeptide #27.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1110
ID ADJ65594 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1111
ID ADL31332 standard; protein; 299 AA.
DE Human protein encoded by a full length cDNA clone seqID 3365.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1112
ID ADM27730 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1113
ID ADL26800 standard; protein; 299 AA.
DE Human JMW protein SEQ ID NO:54.
PN WO2004022778-A1.
PD 18-MAR-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1114
ID ADM42454 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1115
ID ADO06154 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1116
ID ADN35284 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1117
ID ADN05140 standard; protein; 299 AA.
DE Antiporiatic protein sequence #749.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1118
ID ADM28316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1119
ID ADQ95890 standard; protein; 299 AA.
DE T cell activation associated protein #34.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASahi KASEI PHARMA CORP.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1120
ID ADRI1006 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1121
ID ADRI7915 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERE/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILIAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1122
ID ADR27641 standard; protein; 299 AA.
DE Human F11 receptor protein Seq 7.
PN WO2004063327-A2.
PD 29-JUL-2004.
PA (KORN/) KORNECKI E.
PA (BABI/) BABINSKI A.
PA (EHLR/) EHRLICH Y H.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1123
ID ADI95798 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1124
ID ADI96350 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1125
ID ADR46577 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4, SEQ ID 8.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1126
ID ADR46571 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1127
ID ADR46573 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1128
ID ADR46579 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 5.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSHI HOJIN KAGAKU GIJUTSU SH.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1129
ID ADR94260 standard; protein; 299 AA.
DE Human PRO301 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1130
ID ADR574554 standard; protein; 299 AA.
DE Human secreted/transmembrane protein #25.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N P.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1131
ID ADS32302 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1132
ID ADT03286 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1133
ID ADT03591 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1134
ID ADU06480 standard; protein; 299 AA.
DE Novel bronchial cancer-associated human protein SeqID704.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1135
ID ADU06355 standard; protein; 299 AA.
DE Novel bronchial cancer-associated human protein SeqID579.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1136
ID ADU66684 standard; protein; 299 AA.
DE Human platelet F11 receptor protein, F11R-A.
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 25.2%; Score 404; DB 8; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1137
ID ADM97860 standard; protein; 299 AA.
DE Human junctional adhesion molecule-1 (JAM-1) protein.
PN US2005025776-A1.
PD 03-FEB-2005.
PA (WEBE/) WEBER C.
Query Match 25.2%; Score 404; DB 9; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1138
ID ADZ03337 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO301 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 9; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1139

ID AEA37829 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 25.2%; Score 404; DB 9; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1140
ID AEA29245 standard; protein; 299 AA.
DE Human junction adhesion molecule -1 as target for drug delivery method.
PN US2005129679-A1.
PD 16-JUN-2005.
PA (NAST-) NASTECH PHARM CO INC.
Query Match 25.2%; Score 404; DB 9; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1141
ID AEB14083 standard; protein; 299 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 366.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 25.2%; Score 404; DB 9; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.3e-24;
RESULT 1142
ID ADE09073 standard; protein; 320 AA.
DE Novel protein-related contig polypeptide sequence #139.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSE INC.
Query Match 25.2%; Score 404; DB 7; Length 320;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1143
ID ADU40591 standard; protein; 320 AA.
DE Novel human polypeptide seq id 376.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Query Match 25.2%; Score 404; DB 9; Length 320;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1144
ID ADE08038 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #193.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSE INC.
Query Match 25.2%; Score 404; DB 7; Length 336;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1145
ID ADU40408 standard; protein; 336 AA.
DE Novel human polypeptide seq id 193.
PN US2004219521-A1.
PD 04-NOV-2004.
PA (TANG/) TANG Y T.
PA (WANG/) WANG Z.
PA (WENG/) WENG G.
PA (BOYL/) BOYLE B J.
PA (DRMA/) DRMANAC R T.
Query Match 25.2%; Score 404; DB 9; Length 336;
Best Local Similarity 35.2%; Pred. No. 1.5e-24;
RESULT 1146
ID AAY23326 standard; protein; 260 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 2; Length 260;
Best Local Similarity 38.4%; Pred. No. 2e-24;
RESULT 1147
ID AAY08072 standard; protein; 260 AA.
DE Human DNA40628 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 2; Length 260;
Best Local Similarity 38.4%; Pred. No. 2e-24;
RESULT 1148
ID ADH62550 standard; protein; 260 AA.
DE Human PRO301 protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAP1/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 25.0%; Score 401; DB 7; Length 260;
Best Local Similarity 38.4%; Pred. No. 2e-24;
RESULT 1149
ID AAY23328 standard; protein; 263 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 2; Length 263;
Best Local Similarity 38.4%; Pred. No. 2e-24;
RESULT 1150
ID AAY08074 standard; protein; 263 AA.
DE Human DNA40628 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 25.0%; Score 401; DB 2; Length 263;
Best Local Similarity 38.4%; Pred. No. 2e-24;
RESULT 1151
ID ADH62552 standard; protein; 263 AA.
DE Human PRO301 protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAP1/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 25.0%; Score 401; DB 7; Length 263;
Best Local Similarity 38.4%; Pred. No. 2e-24;
RESULT 1152
ID ADJ67616 standard; protein; 335 AA.
DE Human ovarian specific polypeptide SEQ ID NO:330.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 24.6%; Score 395; DB 8; Length 335;

Best Local Similarity 35.7%; Pred. No. 8.4e-24;
RESULT 1153
ID AAW61380 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule protein.
PN W09824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 24.5%; Score 394; DB 2; Length 300;
Best Local Similarity 34.8%; Pred. No. 8.8e-24;
RESULT 1154
ID AAY23325 standard; protein; 300 AA.
DE A33 related antigen JAM.
PN W09927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 24.5%; Score 394; DB 2; Length 300;
Best Local Similarity 34.8%; Pred. No. 8.8e-24;
RESULT 1155
ID ADH62537 standard; protein; 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 24.5%; Score 394; DB 7; Length 300;
Best Local Similarity 34.8%; Pred. No. 8.8e-24;
RESULT 1156
ID ADK40853 standard; protein; 300 AA.
DE Mouse junction adhesion molecule (JAM).
PN U56699688-B1.
PD 02-MAR-2004.
PA (UVNY) UNIV NEW YORK STATE RES FOUND.
Query Match 24.5%; Score 394; DB 8; Length 300;
Best Local Similarity 34.8%; Pred. No. 8.8e-24;
RESULT 1157
ID ADN35293 standard; protein; 300 AA.
DE Human JAM protein.
PN W02004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 24.5%; Score 394; DB 8; Length 300;
Best Local Similarity 34.8%; Pred. No. 8.8e-24;
RESULT 1158
ID ADR46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 24.5%; Score 394; DB 8; Length 300;
Best Local Similarity 34.8%; Pred. No. 8.8e-24;
RESULT 1159
ID ADU66693 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule (JAM).
PN US2004235768-A1.
PD 25-NOV-2004.
PA (KORN/) KORNECKI E.
PA (SOBO/) SOBOCKA M B.
Query Match 24.5%; Score 394; DB 8; Length 300;
Best Local Similarity 34.8%; Pred. No. 8.8e-24;
RESULT 1160
ID ADH80723 standard; protein; 300 AA.
DE Human polypeptide #40.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
Query Match 24.5%; Score 394; DB 7; Length 238;
Best Local Similarity 34.7%; Pred. No. 1.4e-21;
RESULT 1167
ID ADG39449 standard; protein; 238 AA.
DE Human JAM-2 protein SEQ ID NO:18.
PN W02003104400-A2.
PD 18-DEC-2003.

PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match 24.5%; Score 392.5; DB 8; Length 300;
Best Local Similarity 35.1%; Pred. No. 1.2e-23;
RESULT 1161
ID ADH80722 standard; protein; 301 AA.
DE Human polypeptide #39.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match 24.0%; Score 385; DB 8; Length 301;
Best Local Similarity 34.9%; Pred. No. 4.9e-23;
RESULT 1162
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN W0200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.9%; Score 383; DB 3; Length 280;
Best Local Similarity 36.2%; Pred. No. 6.5e-23;
RESULT 1163
ID ADQ95892 standard; protein; 259 AA.
DE T cell activation associated protein #35.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 23.2%; Score 372.5; DB 8; Length 259;
Best Local Similarity 37.3%; Pred. No. 4.2e-22;
RESULT 1164
ID ADR46575 standard; protein; 259 AA.
DE Human JAM-1, Fll receptor (FllR) transcript variant 3.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 23.3%; Score 372.5; DB 8; Length 259;
Best Local Similarity 37.3%; Pred. No. 4.2e-22;
RESULT 1165
ID AAU14169 standard; protein; 259 AA.
DE Human novel protein #40.
PN W0200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.8%; Score 366.5; DB 4; Length 259;
Best Local Similarity 36.8%; Pred. No. 1.3e-21;
RESULT 1166
ID ADF12431 standard; protein; 238 AA.
DE Human adhesion molecule JAM-2.
PN W02003087128-A2.
PD 23-OCT-2003.
PA (RMFD-) RMF DICTAGENE SA.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 22.8%; Score 365.5; DB 7; Length 238;
Best Local Similarity 34.7%; Pred. No. 1.4e-21;
RESULT 1167
ID ADG39449 standard; protein; 238 AA.
DE Human JAM-2 protein SEQ ID NO:18.
PN W02003104400-A2.
PD 18-DEC-2003.

PA (BMPD-) RMP DICTAGENE SA.
PA (UTPE-) UNIV PENNSYLVANIA.
Query Match 22.8%; Score 365.5; DB 8; Length 238;
Best Local Similarity 34.7%; Pred. No. 1.4e-21;
RESULT 1168
ID ADP56685 standard; protein; 265 AA.
DE Human junction adhesion molecule 3 splice variant 2 (huJAM3sv2) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 22.8%; Score 365.5; DB 8; Length 265;
Best Local Similarity 34.7%; Pred. No. 1.6e-21;
RESULT 1169
ID ADU06841 standard; protein; 265 AA.
DE Cell adhesion and extracellular matrix protein clone 7518734CD1.
PN WO2004094623-A2.
PD 04-NOV-2004.
PA (INCY-) INCYTE CORP.
Query Match 22.8%; Score 365.5; DB 8; Length 265;
Best Local Similarity 34.7%; Pred. No. 1.6e-21;
RESULT 1170
ID ABG22339 standard; protein; 69 AA.
DE Novel human diagnostic protein #22330.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.2%; Score 357; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
RESULT 1171
ID ADP69098 standard; protein; 206 AA.
DE Human NOV2a mature extracellular domain protein SEQ ID NO:68.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 22.2%; Score 357; DB 8; Length 206;
Best Local Similarity 36.8%; Pred. No. 5.9e-21;
RESULT 1172
ID ADP69031 standard; protein; 206 AA.
DE Human NOV2d protein SEQ ID NO:26.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 22.2%; Score 357; DB 8; Length 206;
Best Local Similarity 36.8%; Pred. No. 5.9e-21;
RESULT 1173
ID ADP69029 standard; protein; 206 AA.
DE Human NOV2c protein SEQ ID NO:24.
PN WO2004055158-A2.
PD 01-JUL-2004.
PA (CURA-) CURAGEN CORP.
Query Match 22.2%; Score 357; DB 8; Length 206;
Best Local Similarity 36.8%; Pred. No. 5.9e-21;
RESULT 1174
ID AAW61379 standard; protein; 298 AA.
DE Human junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 21.5%; Score 344.5; DB 2; Length 298;
Best Local Similarity 31.8%; Pred. No. 1e-19;
RESULT 1175
ID ADQ65675 standard; protein; 259 AA.
DE Novel human protein sequence #648.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.4%; Score 344; DB 8; Length 259;
Best Local Similarity 30.1%; Pred. No. 9.2e-20;
RESULT 1176
ID ABG22401 standard; protein; 361 AA.
DE Novel human diagnostic protein #22392.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 21.2%; Score 341; DB 4; Length 361;
Best Local Similarity 30.0%; Pred. No. 2.5e-19;
RESULT 1177
ID ABG12109 standard; protein; 404 AA.
DE Novel human diagnostic protein #12100.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 19.0%; Score 304.5; DB 4; Length 404;
Best Local Similarity 27.1%; Pred. No. 2.8e-16;
RESULT 1178
ID ABG04645 standard; protein; 291 AA.
DE Novel human diagnostic protein #4636.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 18.9%; Score 303.5; DB 4; Length 291;
Best Local Similarity 29.6%; Pred. No. 2.2e-16;
RESULT 1179
ID ADP56684 standard; protein; 229 AA.
DE Human junction adhesion molecule 3 splice variant 1 (huJAM3sv1) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL) LILLY & CO ELI.
Query Match 18.7%; Score 300.5; DB 8; Length 229;
Best Local Similarity 33.0%; Pred. No. 2.9e-16;
RESULT 1180
ID AAW74465 standard; protein; 205 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 17.0%; Score 273.5; DB 2; Length 205;
Best Local Similarity 35.1%; Pred. No. 4.1e-14;
RESULT 1181
ID ABG22340 standard; protein; 66 AA.
DE Novel human diagnostic protein #22331.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 16.5%; Score 265; DB 4; Length 66;
Best Local Similarity 98.1%; Pred. No. 4.7e-14;
RESULT 1182
ID ABU69130 standard; protein; 225 AA.
DE Human NOVX polypeptide #5.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.5%; Score 264.5; DB 6; Length 225;
Best Local Similarity 39.0%; Pred. No. 2.5e-13;
RESULT 1183
ID ADO08263 standard; protein; 225 AA.
DE Human NOVX polypeptide #5.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASHMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KERUDA R.
PA (LEPL/) LEPLLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALX/) MALYANKAR U M.
PA (MILL/) MILLER C E.

PA (MILL//) MILLET I.
PA (PADI//) PADIGARU M.
PA (PATT//) PATTURAJAN M.
PA (PENA//) PENA C E A.
PA (RIEG//) RIEGER D K.
PA (SHEN//) SHENOY S G.
PA (SHIM//) SHIMKETS R A.
PA (SPYT//) SPYTEK K A.
PA (TAUP//) TAUPIER R J.
PA (VERN//) VERNET C A M.
PA (VOSS//) VOSS E Z.
PA (ZERH//) ZERHUSEN B D.
Query Match
Best Local Similarity 16.5%; Score 264.5; DB 8; Length 225;
Best Local Similarity 39.0%; Pred. No. 2.5e-13;
RESULT 1184
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 2; Length 268;
Best Local Similarity 29.0%; Pred. No. 4.7e-11;
RESULT 1185
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK//) ASHKENAZI A.
PA (FONG//) FONG S.
PA (GODD//) GODDARD A.
PA (GURN//) GURNEY A L.
PA (NAPI//) NAPIER M A.
PA (TUMA//) TUMAS D.
PA (WOOD//) WOOD W I.
Query Match
Best Local Similarity 14.8%; Score 238; DB 7; Length 268;
Best Local Similarity 29.0%; Pred. No. 4.7e-11;
RESULT 1186
ID AAV23327 standard; protein; 270 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 2; Length 270;
Best Local Similarity 29.0%; Pred. No. 4.7e-11;
RESULT 1187
ID AAY23329 standard; protein; 273 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 2; Length 273;
Best Local Similarity 29.0%; Pred. No. 4.8e-11;
RESULT 1188
ID AAY08075 standard; protein; 273 AA.
DE Human A33 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 2; Length 273;
Best Local Similarity 29.0%; Pred. No. 4.8e-11;
RESULT 1189
ID ADH62553 standard; protein; 273 AA.
DE Human A33 antigenic protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK//) ASHKENAZI A.
PA (FONG//) FONG S.
PA (GODD//) GODDARD A.
PA (GURN//) GURNEY A L.
PA (NAPI//) NAPIER M A.
PA (TUMA//) TUMAS D.
PA (WOOD//) WOOD W I.
Query Match
Best Local Similarity 14.8%; Score 238; DB 8; Length 273;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1190
ID AAW14146 standard; protein; 319 AA.
DE Human A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW//) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 14.8%; Score 238; DB 2; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1191
ID AAY23323 standard; protein; 319 AA.
DE Amino acid sequence of the A33 antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 2; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1192
ID AAB65863 standard; protein; 319 AA.
DE Human A33 protein SEQ ID NO: 67.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL//) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 4; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1193
ID ADA10947 standard; protein; 319 AA.
DE Human cDNA differentially expressed in colon cancer #43 product.
PN US2002160382-A1.
PD 31-OCT-2002.
PA (LASE//) LASEK A W.
PA (JONE//) JONES D A.
Query Match
Best Local Similarity 14.8%; Score 238; DB 6; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1194
ID ADH62533 standard; protein; 319 AA.
DE Human A33 antigenic protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK//) ASHKENAZI A.
PA (FONG//) FONG S.
PA (GODD//) GODDARD A.
PA (GURN//) GURNEY A L.
PA (NAPI//) NAPIER M A.
PA (TUMA//) TUMAS D.
PA (WOOD//) WOOD W I.
Query Match
Best Local Similarity 14.8%; Score 238; DB 7; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1195
ID ADN39847 standard; protein; 319 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C217.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (BOSB//) BOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 7; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1196
ID ADN35289 standard; protein; 319 AA.
DE Human A33 antigen protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 8; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1197
ID ADP54587 standard; protein; 319 AA.
DE Human PRO protein sequence SEQ ID NO: 563.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 8; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1198
ID ADP54587 standard; protein; 319 AA.
DE Human PRO protein sequence SEQ ID NO: 563.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 14.8%; Score 238; DB 8; Length 319;
Best Local Similarity 29.0%; Pred. No. 5.8e-11;
RESULT 1199

ID ABB5134 standard; protein; 319 AA.
 DE Human novel secreted protein hua33.
 PN WO2005058028-A2.
 PD 30-JUN-2005.
 PA (GETH) GENENTECH INC.
 PA (LEXI-) LEXICON GENETICS INC.
 Query Match 14.8%; Score 238; DB 9; Length 319;
 Best Local Similarity 29.0%; Pred. No. 5.8e-11;
 RESULT 1199
 ID ABP6281 standard; protein; 336 AA.
 DE Human polypeptide SEQ ID NO 318.
 PN WO200218424-A2.
 PD 07-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match 14.8%; Score 238; DB 5; Length 336;
 Best Local Similarity 29.0%; Pred. No. 6.2e-11;
 RESULT 1200
 ID ADK40854 standard; protein; 316 AA.
 DE Human A33 molecule.
 PN US6699688-B1.
 PD 02-MAR-2004.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 Query Match 14.6%; Score 234.5; DB 8; Length 316;
 Best Local Similarity 28.9%; Pred. No. 1.1e-10;
 RESULT 1201
 ID ADU66694 standard; protein; 316 AA.
 DE Human A33 protein.
 PN US2004235768-A1.
 PD 25-NOV-2004.
 PA (KORV/) KORNECKI E.
 PA (SOBO/) SOBOCKA M B.
 Query Match 14.6%; Score 234.5; DB 8; Length 316;
 Best Local Similarity 28.9%; Pred. No. 1.1e-10;
 RESULT 1202
 ID ADK40845 standard; protein; 193 AA.
 DE Human platelet F11 receptor #2.
 PN US6699688-B1.
 PD 02-MAR-2004.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 Query Match 14.0%; Score 224.5; DB 8; Length 193;
 Best Local Similarity 34.9%; Pred. No. 3.9e-10;
 RESULT 1203
 ID ADU66685 standard; protein; 193 AA.
 DE Human platelet F11 receptor protein, F11R-B.
 PN US2004235768-A1.
 PD 25-NOV-2004.
 PA (KORV/) KORNECKI E.
 PA (SOBO/) SOBOCKA M B.
 Query Match 14.0%; Score 224.5; DB 8; Length 193;
 Best Local Similarity 34.9%; Pred. No. 3.9e-10;
 RESULT 1204
 ID ADW97861 standard; protein; 88 AA.
 DE Human JAM-1 protein active fragment.
 PN US2005025776-A1.
 PD 03-FEB-2005.
 PA (WEBE/) WEBER C.
 Query Match 13.8%; Score 221; DB 9; Length 88;
 Best Local Similarity 49.4%; Pred. No. 2.8e-10;
 RESULT 1205
 ID AAW14158 standard; protein; 318 AA.
 DE Mouse A33 antigen.
 PN WO9708189-A1.
 PD 06-MAR-1997.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 13.6%; Score 219; DB 2; Length 318;
 Best Local Similarity 26.9%; Pred. No. 2.1e-09;
 RESULT 1206
 ID ADC78359 standard; protein; 389 AA.
 DE Human PRO246 protein.
 PN WO200015796-A2.
 PD 23-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 13.3%; Score 213.5; DB 3; Length 389;
 Best Local Similarity 29.1%; Pred. No. 7.7e-09;
 RESULT 1207
 ID ADO43535 standard; protein; 348 AA.
 DE Amino acid sequence of an additional human A34 clone.
 PN WO2004037999-A2.
 PD 06-MAY-2004.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 13.2%; Score 211.5; DB 8; Length 348;
 Best Local Similarity 25.8%; Pred. No. 9.7e-09;
 RESULT 1208
 ID ADP5948 standard; protein; 370 AA.
 DE Human PRO protein sequence SEQ ID NO:1924.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 13.2%; Score 211.5; DB 8; Length 370;
 Best Local Similarity 25.8%; Pred. No. 1.1e-08;
 RESULT 1209
 ID AAY08621 standard; protein; 387 AA.
 DE Human secreted protein AJ26_3.
 PN WO9926972-A1.
 PD 03-JUN-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 13.2%; Score 211.5; DB 2; Length 387;
 Best Local Similarity 25.8%; Pred. No. 1.1e-08;
 RESULT 1210
 ID AAY67312 standard; protein; 387 AA.
 DE Human secreted protein AJ26_3 amino acid sequence.
 PN WO9960020-A1.
 PD 25-NOV-1999.
 PA (GEMY) GENETICS INST INC.
 Query Match 13.2%; Score 211.5; DB 3; Length 387;
 Best Local Similarity 25.8%; Pred. No. 1.1e-08;
 RESULT 1211
 ID ADC38775 standard; protein; 387 AA.
 DE Human secreted protein #62.
 PN US2002193567-A1.
 PD 19-DEC-2002.
 PA (GEMY) GENETICS INST INC.
 Query Match 13.2%; Score 211.5; DB 7; Length 387;
 Best Local Similarity 25.8%; Pred. No. 1.1e-08;
 RESULT 1212
 ID ADO43531 standard; protein; 387 AA.
 DE Amino acid sequence of a full length human A34 protein.
 PN WO2004037999-A2.
 PD 06-MAY-2004.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 13.2%; Score 211.5; DB 8; Length 387;
 Best Local Similarity 25.8%; Pred. No. 1.1e-08;
 RESULT 1213
 ID ADO43533 standard; protein; 402 AA.
 DE Amino acid sequence of a human A34 protein.
 PN WO2004037999-A2.
 PD 06-MAY-2004.
 PA (LUDW-) LUDWIG INST CANCER RES.
 Query Match 13.2%; Score 211.5; DB 8; Length 402;
 Best Local Similarity 25.8%; Pred. No. 1.2e-08;
 RESULT 1214
 ID AAY76303 standard; protein; 389 AA.
 DE Fragment of human secreted protein encoded by gene 29.
 PN WO9958660-A1.
 PD 18-NOV-1999.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 13.1%; Score 211; DB 3; Length 389;
 Best Local Similarity 27.9%; Pred. No. 1.2e-08;
 RESULT 1215
 ID ADE11956 standard; protein; 389 AA.
 DE Human secreted polypeptide #210.
 PN US2003100051-A1.
 PD 29-MAY-2003.
 PA (RUBE/) RUBEN S M.
 PA (FLOR/) FLORENCE K A.
 PA (NIJJ/) NI J.

PA (ROSE/) ROSEN C A.
 PA (CART/) CARTER K C.
 PA (MOOR/) MOORE P A.
 PA (OLSE/) OLSEN H S.
 PA (SHIY/) SHI Y.
 PA (YOUN/) YOUNG P E.
 PA (WEIY/) WEI Y.
 PA (BREW/) BREWER L A.
 PA (SOPP/) SOPPET D R.
 PA (LAF/) LAFLEUR D W.
 PA (ENDR/) ENDRESS G A.
 PA (EBNE/) EBNER R.
 PA (BIRS/) BIRSE C E.
 Query Match 13.1%; Score 211; DB 7; Length 389;
 Best Local Similarity 27.9%; Pred. No. 1.2e-08;
 RESULT 1216
 ID ADC42841 standard; protein; 423 AA.
 DE REMAP protein #1.
 PN WO2003027228-A2.
 PD 03-APR-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 13.1%; Score 211; DB 7; Length 423;
 Best Local Similarity 24.5%; Pred. No. 1.4e-08;
 RESULT 1217
 ID AAB90818 standard; protein; 390 AA.
 DE Human shear stress-response protein SEQ ID NO: 144.
 PN WO200125427-A1.
 PD 12-APR-2001.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PA (NOJI/) NOJIMA H.
 Query Match 13.1%; Score 210.5; DB 4; Length 390;
 Best Local Similarity 26.3%; Pred. No. 1.4e-08;
 RESULT 1218
 ID AAY05286 standard; protein; 390 AA.
 DE EGF-like homologue PRO246.
 PN WO9914327-A2.
 PD 25-MAR-1999.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 2; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1219
 ID AAY13351 standard; protein; 390 AA.
 DE Amino acid sequence of protein PRO246.
 PN WO9914328-A2.
 PD 25-MAR-1999.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 2; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1220
 ID AAY27096 standard; protein; 390 AA.
 DE Human viral receptor protein (ACVRP).
 PN US942606-A.
 PD 24-AUG-1999.
 PA (INCY-) INCYTE PHARM INC.
 Query Match 13.1%; Score 210; DB 2; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1221
 ID AAY94999 standard; protein; 390 AA.
 DE Human secreted protein vcs1_1, SEQ ID NO:38.
 PN WO20011015-A1.
 PD 02-MAR-2000.
 PA (ALPH-) ALPHAGEN INC.
 Query Match 13.1%; Score 210; DB 3; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1222
 ID AAY88574 standard; protein; 390 AA.
 DE Human PRO246 amino acid sequence.
 PN WO200015666-A2.
 PD 23-MAR-2000.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 3; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1223
 ID AAB80219 standard; protein; 390 AA.
 DE Human PRO246 protein.
 PN WO200104311-A1.
 PD 18-JAN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 4; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1224
 ID AAE06610 standard; protein; 390 AA.
 DE Human protein having hydrophobic domain, HP10801.
 PN WO200149728-A2.
 PD 12-JUL-2001.
 PA (PROT-) PROTEGENE INC.
 PA (SAGA) SAGAMI CHEM RES CENT.
 Query Match 13.1%; Score 210; DB 4; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1225
 ID AAB31207 standard; protein; 390 AA.
 DE Amino acid sequence of human polypeptide PRO246.
 PN WO200077037-A2.
 PD 21-DEC-2000.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 4; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1226
 ID AAU12340 standard; protein; 390 AA.
 DE Human PRO246 polypeptide sequence.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 4; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1227
 ID AAB53082 standard; protein; 390 AA.
 DE Human angiogenesis-associated protein PRO246, SEQ ID NO:96.
 PN WO200053753-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 4; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1228
 ID AAB68599 standard; protein; 390 AA.
 DE PRO246.
 PN WO200105836-A1.
 PD 25-JAN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 4; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1229
 ID AAB88358 standard; protein; 390 AA.
 DE Human membrane or secretory protein clone PSEC0086.
 PN EP1067182-A2.
 PD 10-JAN-2001.
 PA (HELI-) HELIX RES INST.
 Query Match 13.1%; Score 210; DB 4; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1230
 ID ABU71597 standard; protein; 390 AA.
 DE Human PRO polypeptide #8.
 PN US2002146709-A1.
 PD 10-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 6; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1231
 ID ABO17784 standard; protein; 390 AA.
 DE Novel human secreted and transmembrane protein PRO246.
 PN US2003032156-A1.
 PD 13-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 13.1%; Score 210; DB 6; Length 390;
 Best Local Similarity 27.9%; Pred. No. 1.5e-08;
 RESULT 1232

ID ABU71452 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1233
ID ADA56949 standard; protein; 390 AA.
DE Human secreted protein #232.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1234
ID ABO25178 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1235
ID ABU81038 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1236
ID ABU71898 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1237
ID ABO01781 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2002197671-A1.
PD 28-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1238
ID ABU66738 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1239
ID ABU54354 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1240
ID ADA40800 standard; protein; 390 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1241
ID ABU67296 standard; protein; 390 AA.
DE Human secreted / transmembrane polypeptide PRO246.

DE Novel human secreted and transmembrane protein PRO246.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1242
ID ABO47369 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1243
ID ABR47754 standard; protein; 390 AA.
DE Human secreted protein, SEQ ID 645.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1244
ID ABU59819 standard; protein; 390 AA.
DE Novel secreted and transmembrane protein PRO246.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1245
ID ABO25009 standard; protein; 390 AA.
DE Human secreted/transmembrane protein (PRO) #169.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1246
ID ABU64506 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1247
ID ABU72064 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1248
ID ABU67352 standard; protein; 390 AA.
DE Human secreted protein PRO246.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1249
ID ABU67165 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1250
ID ABO14872 standard; protein; 390 AA.
DE Human secreted / transmembrane polypeptide PRO246.

PN US200303060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1251
ID ABU67014 standard; protein; 390 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 338.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1252
ID ABU69629 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1253
ID ABU79807 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1254
ID ABO14811 standard; protein; 390 AA.
DE Human secreted / transmembrane polypeptide PRO246.
PN US2003027143-A1.
PD 08-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1255
ID ADA45857 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1256
ID ADA76288 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1257
ID ADB29244 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1258
ID ADA19938 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1259
ID ADA61561 standard; protein; 390 AA.
DE Homo sapiens.
PN US2003049816-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1260
ID ADB19346 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1261
ID ADB27887 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1262
ID ADA86366 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1263
ID ADB15930 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1264
ID ADA47716 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1265
ID ADA18100 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1266
ID ABO32763 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1267
ID ADA67511 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1268
ID ADB30518 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068794-A1.
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1269
ID ADA85814 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1270
ID ADA97026 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1271
ID ADA9330 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1272
ID ADA87469 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1273
ID ADB16671 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1274
ID ABO34823 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1275
ID ADA16075 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1276
ID ADA91763 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1277
ID ADB14826 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1278
ID ADA47282 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1279
ID ADB18787 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1280
ID ADA94002 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1281
ID ADB19898 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1282
ID ADB13210 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1283
ID ABO43317 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1284
ID ADA74464 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1285
ID ADA42220 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1286
ID ADB24697 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
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Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1287
ID ADA82221 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1288
ID ADA75184 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1289
ID ADA85262 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1290
ID ADA84710 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1291
ID ABO53064 standard; protein; 390 AA.
DE Human putative spliceosome associated protein (SAP) #41.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1292
ID ABO17501 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1293
ID ADB29966 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1294
ID ADA80494 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1295
ID ADA75736 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;

Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1296
ID ADA46961 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1297
ID ADB25257 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1298
ID ADA93433 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1299
ID ADB26783 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1300
ID ADB31070 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1301
ID ADA60998 standard; protein; 390 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1302
ID ADB24145 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1303
ID ADA96474 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1304
ID ADA81046 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;

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RESULT 1305
ID ADA95922 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1306
ID ADB26231 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1307
ID ADB21716 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 6; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1308
ID ADA77495 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1309
ID ADB18235 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1310
ID ADA86918 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1311
ID ADA16499 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1312
ID ADA12928 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1313
ID ADA41796 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1314
ID ADA88021 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1315
ID ADA46409 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1316
ID ADA17143 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1317
ID ADA42646 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1318
ID ADB28439 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1319
ID ADB28991 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1320
ID ADA76943 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1321
ID ADA88573 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1322
ID ADA97578 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1323
ID ADB27335 standard; protein; 390 AA.
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DE Human PRO polypeptide #169.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1324
ID ADB22268 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1325
ID ABO19865 standard; protein; 390 AA.
DE Human secreted/transmembrane protein PRO246.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1326
ID ABO17562 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1327
ID ADA66959 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1328
ID ADB22820 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1329
ID ADB23593 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1330
ID ADA92315 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1331
ID ADB15378 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1332
ID ADB38630 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082766-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1333
ID ADB38078 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1334
ID ADB66550 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1335
ID ADB89630 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1336
ID ADB90362 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1337
ID ADB77565 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1338
ID ADB39463 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1339
ID ADB74701 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1340
ID ADB47086 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1341
ID ADB86693 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1342
ID ADB77298 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1343
ID ADB34455 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1344
ID ADB35559 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1345
ID ADB33903 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1346
ID ADB35007 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1347
ID ADB36111 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1348
ID ADB46506 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1349
ID ADC28347 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1350
ID ADC39547 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1351
ID ADC40061 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1352
ID ADC18889 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1353
ID ADC34185 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1354
ID ADC29240 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1355
ID ADC28771 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1356
ID ADC40656 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1357
ID ADC19313 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1358
ID ADC33761 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1359
ID ADC12831 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
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RESULT 1360
ID ADC50379 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1361
ID ADC71926 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1362
ID ADC59905 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1363
ID ADC52912 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1364
ID ADC57266 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1365
ID ADC60457 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1366
ID ADC50932 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1367
ID ADC65459 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1368
ID ADC54557 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1369
ID ADD09992 standard; protein; 390 AA.

ID ADC53518 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1370
ID ADC59041 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1371
ID ADC55919 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1372
ID ADC58489 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein Seq ID338.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1373
ID ADC12283 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1374
ID ADD03163 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1375
ID ADC90155 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1376
ID ADC69574 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1377
ID ADC48463 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1378
ID ADD09992 standard; protein; 390 AA.

DE Human PRO polypeptide #169.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1379
ID ADD04567 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1380
ID ADC80523 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1381
ID ADD11030 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1382
ID ADC47911 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1383
ID ADD04838 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1384
ID ADC79971 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1385
ID ADD09440 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1386
ID ADD03844 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1387
ID ADD03420 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.

PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1388
ID ADD41153 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1389
ID ADD52292 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1390
ID ADD53032 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1391
ID ADD53584 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1392
ID ADD51740 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1393
ID ADD02539 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1394
ID ADD01973 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1395
ID ADD54155 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1396
ID ADD92472 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199030-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1397
ID ADE91368 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1398
ID ADE03982 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1399
ID ADE32279 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1400
ID ADE22211 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1401
ID ADD79435 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1402
ID ADE41971 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1403
ID ADE17788 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1404
ID ADD91920 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1405
ID ADE33383 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194767-A1.
PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1406
ID ADE33935 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1407
ID ADD79987 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1408
ID ADD93024 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1409
ID ADE19444 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1410
ID ADE34672 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1411
ID ADE18892 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1412
ID ADE43088 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1413
ID ADD95877 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1414
ID ADE22763 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1415				
ID ADH78881 standard; protein; 390 AA.				
DE Human PRO polypeptide #169.				
FN US2003203429-A1.				
PD 30-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1416				
ID ADP32831 standard; protein; 390 AA.				
DE Novel human secreted and transmembrane protein PRO246.				
FN US2003194766-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1417				
ID ADE42523 standard; protein; 390 AA.				
DE Human PRO polypeptide #169.				
FN US2003199032-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1418				
ID ADP80539 standard; protein; 390 AA.				
DE Human PRO polypeptide #169.				
FN US2003207418-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1419				
ID ADP89567 standard; protein; 390 AA.				
DE Human PRO polypeptide #169.				
FN US2003199028-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1420				
ID ADE40851 standard; protein; 390 AA.				
DE Human PRO polypeptide #169.				
FN US2003199031-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1421				
ID ADE04650 standard; protein; 390 AA.				
DE Human PRO polypeptide #169.				
FN US2003199034-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1422				
ID ADE92779 standard; protein; 390 AA.				
DE Human PRO polypeptide #169.				
FN US2003194777-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1423				
ID ADE92779 standard; protein; 390 AA.				
DE Human PRO polypeptide #169.				
FN US2003194777-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1424				
ID ADG21488 standard; protein; 390 AA.				
DE Novel human secreted and transmembrane protein PRO246.				
FN US2003207355-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1425				
ID ADG21488 standard; protein; 390 AA.				
DE Novel human secreted and transmembrane protein PRO246.				
FN US2003207355-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1426				
ID ADG21488 standard; protein; 390 AA.				
DE Novel human secreted and transmembrane protein PRO246.				
FN US2003207355-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	13.1%;	Score 210;	DB 7;	Length 390;
Best Local Similarity	27.9%;	Pred. No. 1.5e-08;		
RESULT 1427				

RESULT 1433
ID AD164039 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1434
ID AD164988 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1435
ID AD163487 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1436
ID ADH81901 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1437
ID ADH81349 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1438
ID ADJ26202 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1439
ID ADM82518 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1440
ID ADN15917 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1441
ID ADN16546 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1442
ID ADN15365 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1443
ID ADN14813 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 7; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1444
ID ADC81075 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1445
ID ADE79117 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1446
ID AD76523 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1447
ID ADD87887 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1448
ID ADD86291 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1449
ID ADE79541 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1450
ID ADE75739 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1451
ID ADE73217 standard; protein; 390 AA.

DE Human secreted/transmembrane protein, #9.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1452
ID ADE23315 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1453
ID ADE23867 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1454
ID ADE24510 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1455
ID ADE89201 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1456
ID ADE89201 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1457
ID ADE41205 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1458
ID ADE73752 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1459
ID ADE18340 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1460
ID ADE88649 standard; protein; 390 AA.
DE Human PRO polypeptide #169.

PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1461
ID ADE99306 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1462
ID ADE94669 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1463
ID ADE91080 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1464
ID ADE95221 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1465
ID ADE93331 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1466
ID ADF34912 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1467
ID ADE98425 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1468
ID ADE92227 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1469
ID ADE90528 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199063-A1.


```
RESULT 1487
ID ADG08344 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1488
ID ADG15514 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1489
ID ADF65912 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1490
ID ADG06097 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1491
ID ADG23681 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1492
ID ADG03970 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1493
ID ADG24871 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1494
ID ADG07168 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1495
ID ADG07720 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1496
ID ADG55215 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1497
ID ADG60879 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1498
ID ADG61983 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1499
ID ADG92135 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
RESULT 1500
ID ADG82184 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 13.1%; Score 210; DB 8; Length 390;
Best Local Similarity 27.9%; Pred. No. 1.5e-08;
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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:42:34 ; Search time 16 seconds
(without alignments)
1876.227 Million cell updates/sec

Title: US-10-785-607C-9

Perfect score: 1605

Sequence: 1 MARRSRRLLLLLRLVVA.....TPVIPALWKAAGSRGQEF 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404	25.2	229	2 S56749	junctional adhesio
2	206.5	12.9	365	2 JC7780	coxsackie- and ade
3	184	11.5	811	2 A41054	fasciclin II, tran
4	184	11.5	873	2 B41054	fasciclin II PI-II
5	177	11.0	6642	2 T29757	protein UNC-89 - C
6	169.5	10.6	7962	2 I38346	elastic titin - hu
7	162	10.1	725	2 JE0100	neural cell adhesi
8	162	10.1	1367	2 A41228	protein-tyrosine k
9	161	10.0	344	2 A27681	nonspecific cross-
10	158	9.8	1092	1 JN0635	neural cell adhesi
11	157	9.8	860	2 JC5702	Erbb kinase activa
12	157	9.8	868	2 JC5701	Erbb kinase activa
13	156	9.7	1897	1 TDHULK	leukocyte antigen-
14	155.5	9.7	1328	2 T23007	hypothetical prote
15	155.5	9.7	2783	2 T34416	hypothetical prote
16	155	9.7	521	2 JC1508	biliary glycoprote
17	155	9.7	725	2 JE0099	neural cell adhesi
18	155	9.7	850	2 JC5700	Erbb kinase activa
19	155	9.7	1088	1 IJXLMN	neural cell adhesi
20	154.5	9.6	1323	2 PN0368	connectin 3B - chi
21	154.5	9.6	4391	2 A38096	perlecan precursor
22	153	9.5	4162	2 T42633	connectin/titin -
23	152.5	9.5	1091	1 IJCHNL	neural cell adhesi
24	152	9.5	1033	2 S19247	cell adhesion prot
25	152	9.5	1239	1 A32579	neuroglian - fruit
26	152	9.5	5175	2 T20992	hypothetical prote
27	152	9.5	5198	2 T43290	hemichatin precurs
28	151.5	9.4	352	2 T33433	hypothetical prote
29	151.5	9.4	521	2 S34338	biliary glycoprote

neural cell adhesi
CDO protein - huma
hypothetical prote
ecto-ATPase precur
kinase-like protei
hypothetical prote
protein-tyrosine-p
protein-tyrosine-p
leukocyte antigen-
carcinoembryonic a
neural cell adhesi
protein-tyrosine-p
protein-tyrosine-p
neural cell adhesi
vascular endotheli
amalgam protein pr
protein-tyrosine-p
biliary glycoprote
transmembrane rece
dutt1 protein - mo
biliary glycoprote
transmembrane carc
biliary glycoprote
irregular chiasm C
neural cell adhesi
hypothetical prote
sax-3 protein - Ca
heparan sulfate pr
neural cell adhesi
neural cell adhesi
biliary glycoprote
carcinoembryonic a
carcinoembryonic a
CDO protein - rat
protein-tyrosine-p
C-CAM2a protein is
B-cell adhesion pr
neurotrophin - rat
class II histocomp
cell-adhesion mole
B-cell adhesion pr
differentiation an
CD22 homolog/B lym
receptor tyrosine
ror-related recept
protein-tyrosine-p
protein-tyrosine-p
brain-derived neur
brain-derived neur
hypothetical prote
frazzled gene prot
frazzled gene prot
fibroblast growth
biliary glycoprote
rig-1 protein - mo
brain-derived neur
butyrophilin - bov
myosin-light-chain
brain-derived neur
contactin precurs
hypothetical prote
limbic-system-asso
brain-derived neur
fibroblast growth
brain-derived neur
plasmacytoma-asso
Fit-1 tyrosine kin
fibroblast growth
tumor suppressor -
unc-5 protein - Ca
unc-5 protein, lon

103	132.5	8.3	331	2	JH0395	biliary glycoprote	176	121.5	7.6	428	2	JS0032	pregnancy-specific
104	132.5	8.3	800	1	TVH02F	fibroblast growth	177	121.5	7.6	435	2	D33258	pregnancy-specific
105	132.5	8.3	800	2	A48991	heparin-binding gr	178	121.5	7.6	816	2	A49151	fibroblast growth
106	132.5	8.3	801	2	I55363	fibroblast growth	179	121.5	7.6	898	2	A40114	fascilin II precu
107	132.5	8.3	1356	2	J14102	protein-tyrosine k	180	121	7.5	182	2	A34647	pregnancy-specific
108	132	8.2	1333	2	I78875	receptor tyrosine	181	121	7.5	361	2	PN0020	fibroblast growth
109	132	8.2	1348	2	S51556	vascular endotheli	182	121	7.5	769	2	S16236	fibroblast growth
110	131.5	8.2	309	2	I49522	gene B7-2 protein	183	121	7.5	822	2	A45081	fibroblast growth
111	131.5	8.2	538	2	JC2457	vascular cell adhe	184	121	7.5	822	2	A41794	keratinocyte growt
112	131.5	8.2	976	2	T29583	hypothetical prote	185	121	7.5	832	2	JH0393	fibroblast growth
113	131.5	8.2	1015	2	T32186	hypothetical prote	186	121	7.5	1018	2	JC4211	neural adhesion pr
114	131	8.2	1036	2	S22383	axolin 1 precursor	187	120.5	7.5	799	2	S18209	fibroblast growth
115	129	8.0	769	1	QRR7GS	secretory componen	188	120.5	7.5	821	1	TVHUF2	fibroblast growth
116	129	8.0	871	1	I48696	protein-tyrosine k	189	120.5	7.5	2222	2	T13924	sdk protein - frui
117	129	8.0	881	1	I48697	protein-tyrosine k	190	120	7.5	238	2	T22098	hypothetical prote
118	129	8.0	1535	2	S46224	peroxidasin - frui	191	120	7.5	335	2	A33514	pregnancy-specific
119	129	8.0	6831	2	A88952	protein unc-22 [im	192	120	7.5	662	2	C40862	heparin-binding gr
120	129	8.0	6839	2	S57242	twitchin [similar	193	120	7.5	822	1	TVHUGF	fibroblast growth
121	129	8.0	7160	2	T27935	hypothetical prote	194	120	7.5	822	1	TVMSFG	fibroblast growth
122	128.5	8.0	272	2	I48268	biliary glycoprote	195	120	7.5	822	2	I42889	fibroblast growth
123	128.5	8.0	480	2	B56182	fibroblast growth	196	120	7.5	822	2	S29840	fibroblast growth
124	128.5	8.0	757	2	I45956	polymeric immunogl	197	119.5	7.4	286	2	A28333	carcinoembryonic a
125	128.5	8.0	772	2	T13078	KIAA0992 protein -	198	119.5	7.4	309	2	I49503	B-lymphocyte activ
126	128	8.0	1363	2	I58375	protein-tyrosine k	199	119.5	7.4	338	2	JC1238	opioid-binding pro
127	127.5	7.9	222	2	T43027	neural cell adhesi	200	119.5	7.4	345	2	JC1239	opioid-binding pro
128	126.5	7.9	212	2	C33258	pregnancy-specific	201	119	7.4	310	2	JO1119	Fc gamma (IgG) rec
129	126.5	7.9	419	2	B54312	pregnancy-specific	202	119	7.4	323	2	S06946	Fc gamma (IgG) rec
130	126.5	7.9	419	2	JC4123	pregnancy-specific	203	119	7.4	707	2	A54846	fibroblast growth
131	126.5	7.9	875	2	T33434	hypothetical prote	204	119	7.4	765	2	C42632	cell adhesion mole
132	126.5	7.9	1447	2	A54100	tumor suppressor p	205	119	7.4	812	2	B42632	cell adhesion mole
133	126	7.9	228	2	S29575	Ig light chain - r	206	119	7.4	932	2	A42632	cell adhesion mole
134	126	7.9	338	2	SC5519	50k glycoprotein p	207	119	7.4	1018	2	A54744	contactin 1 precu
135	126	7.9	1338	2	SO9982	protein-tyrosine k	208	119	7.4	3488	2	T34418	hypothetical prote
136	125.5	7.8	326	2	JC4124	pregnancy-specific	209	118.5	7.4	254	2	C42691	fibroblast growth
137	125.5	7.8	341	2	JC1512	biliary glycoprote	210	118.5	7.4	282	2	T17219	hypothetical prote
138	125.5	7.8	352	2	I77174	pregnancy-specific	211	118.5	7.4	317	2	JO1118	Fc gamma (IgG) rec
139	125.5	7.8	480	2	A56182	fibroblast growth	212	118.5	7.4	646	2	I38049	cell surface glyco
140	125.5	7.8	806	1	TVHUF3	fibroblast growth	213	118.5	7.4	739	2	A41288	vascular cell adhe
141	125	7.8	1197	2	T30581	neural cell adhesi	214	118.5	7.4	1443	2	I50600	neogenin - chicken
142	124.5	7.8	210	2	JC4122	pregnancy-specific	215	118.5	7.4	1694	2	S00065	sialoadhesin - mou
143	124.5	7.8	235	2	S20000	Ig light chain pre	216	118.5	7.4	6658	2	T13931	projectin - fruit
144	124.5	7.8	335	2	A43354	pregnancy-specific	217	118	7.4	326	2	F43354	pregnancy-specific
145	124.5	7.8	337	2	C43354	pregnancy-specific	218	118	7.4	567	2	S29498	lymphocyte antigen
146	124.5	7.8	406	2	A43354	pregnancy-specific	219	118	7.4	584	2	T08678	hypothetical prote
147	124.5	7.8	417	2	A28277	pregnancy-specific	220	118	7.4	6805	2	S02901	titin - rabbit (fr
148	124.5	7.8	426	2	A35964	pregnancy-specific	221	117.5	7.3	278	2	JC1506	biliary glycoprote
149	124.5	7.8	822	2	B54846	fibroblast growth	222	117.5	7.3	278	2	A39037	carcinoembryonic a
150	124.5	7.8	1241	2	T37190	nephrin - human	223	117	7.3	509	2	JC5288	SHP substrate-1 pr
151	124	7.7	1028	2	I58164	BiG-1 protein - ra	224	117	7.3	513	2	JC5289	SHP substrate-1 pr
152	124	7.7	1259	2	A43425	Bravo/Nr-CAM cell	225	117	7.3	1040	2	A34695	axonal glycoprotei
153	124	7.7	1268	1	A39640	neural cell adhesi	226	116.5	7.3	333	2	A43354	pregnancy-specific
154	123.5	7.7	273	2	B28928	pregnancy-specific	227	116.5	7.3	345	2	JC4025	opioid-binding cel
155	123.5	7.7	275	2	A28928	pregnancy-specific	228	116.5	7.3	345	2	S03199	opioid-binding pro
156	123.5	7.7	282	2	C28928	pregnancy-specific	229	116.5	7.3	402	2	A54312	pregnancy-specific
157	123.5	7.7	299	2	I46690	CD80 precursor - r	230	116.5	7.3	424	2	B36109	pregnancy-specific
158	123.5	7.7	419	2	A33258	pregnancy-specific	231	116.5	7.3	426	2	C55181	pregnancy-specific
159	123.5	7.7	419	2	A31135	pregnancy-specific	232	116.5	7.3	426	2	B35334	pregnancy-specific
160	123.5	7.7	426	2	B33258	pregnancy-specific	233	116.5	7.3	436	2	B55181	pregnancy-specific
161	123.5	7.7	426	2	A35341	pregnancy-specific	234	116.5	7.3	495	2	A55181	pregnancy-specific
162	123.5	7.7	428	2	A27658	pregnancy-specific	235	116.5	7.3	739	2	JS0675	vascular cell adhe
163	123.5	7.7	757	1	S48841	secretory componen	236	116.5	7.3	764	1	QRHUGS	secretory componen
164	123.5	7.7	26936	1	I38344	titin, cardiac mus	237	116.5	7.3	1123	2	S36846	myosin-binding pro
165	123	7.7	1040	2	A49356	transient axonal g	238	116.5	7.3	1265	1	A37967	neural cell adhesi
166	123	7.7	1091	2	A85332	glial cell membran	239	116	7.2	335	2	C54312	pregnancy-specific
167	123	7.7	1330	2	S49010	embryonic receptor	240	116	7.2	335	2	B33251	non-specific cross-
168	122.5	7.6	419	2	A36109	pregnancy-specific	241	116	7.2	662	2	T16525	hypothetical prote
169	122.5	7.6	1896	2	T08851	Down syndrome cell	242	116	7.2	707	2	A38429	keratinocyte growt
170	122	7.6	682	2	A35969	heparin-binding gr	243	116	7.2	940	2	A40985	pregnancy-specific
171	122	7.6	813	1	A49123	fibroblast growth	244	115.5	7.2	324	2	G43354	pregnancy-specific
172	121.5	7.6	233	2	S29577	Ig light chain - r	245	115.5	7.2	335	2	H43354	neu differentiatio
173	121.5	7.6	332	2	JN0067	pregnancy-specific	246	115.5	7.2	636	2	I61718	fibroblast growth
174	121.5	7.6	424	2	A34595	pregnancy-specific	247	115.5	7.2	824	2	S36439	ufo protein - mous
175	121.5	7.6	428	2	I57486	pregnancy-specific	248	115.5	7.2	888	2	S23065	

249	115.5	7.2	942	2	S23251	protein-tyrosine k	322	106.5	6.6	473	2	D88976	protein F54E2.4 [1
250	115	7.2	351	2	B34595	pregnancy-specific	323	106.5	6.6	538	2	I68093	PRR2 delta - human
251	115	7.2	602	2	A45769	acetylcholine rece	324	106.5	6.6	1011	2	T13669	neuromusculin - fr
252	115	7.2	823	2	B35963	protein-tyrosine k	325	106	6.6	531	2	S20900	titin - mouse (fra
253	115	7.2	824	2	T48108	protein-tyrosine k	326	105.5	6.6	166	2	A33402	pregnancy-specific
254	115	7.2	917	2	I48950	telencephalin prec	327	105.5	6.6	773	1	ORRBG	secretory componen
255	115	7.2	1257	1	A41060	neural cell adhesi	328	105	6.5	240	2	S01299	OX-45 membrane gly
256	115	7.2	1298	2	A48999	protein-tyrosine k	329	104.5	6.5	518	2	JC4024	poliovirus recepto
257	114.5	7.1	413	2	S65948	hemolin - cecropia	330	104.5	6.5	645	2	B43273	herregulin, splice
258	114.5	7.1	426	2	S09016	pregnancy-specific	331	104.5	6.5	789	2	T28714	hypothetical prote
259	114.5	7.1	819	1	TVCHFG	fibroblast growth	332	104.5	6.5	1355	2	T28715	hypothetical prote
260	114.5	7.1	821	1	TVMSBK	fibroblast growth	333	104.5	6.5	1450	2	ADDFLK	165K myofibrillar
261	114	7.1	182	2	I83053	pregnancy-specific	334	104.5	6.5	2029	1	TDFPLK	protein-tyrosine-p
262	114	7.1	206	2	A40305	biliary glycoprote	335	104	6.5	336	2	A42632	Fit-1S protein pre
263	114	7.1	1260	1	S05479	neural cell adhesi	336	104	6.5	344	2	A41357	PC gamma (IgG) rec
264	114	7.1	1274	2	S55050	cardiac myosin-bin	337	104	6.5	353	2	S51242	heparin-binding fi
265	113.5	7.1	392	1	RHUPDA	poliovirus recepto	338	104	6.5	355	2	I51157	major histocompat
266	113.5	7.1	417	1	RHUPDA	poliovirus recepto	339	104	6.5	374	1	A39878	PC gamma (IgG) rec
267	113.5	7.1	524	2	S35341	kettin - fruit fly	340	104	6.5	392	2	B44194	poliovirus recepto
268	113.5	7.1	620	2	JH0593	Schwann cell myeli	341	104	6.5	417	2	A44194	poliovirus recepto
269	113.5	7.1	628	2	I38000	Lutheran blood gro	342	104	6.5	739	2	JN0581	vascular cell adhe
270	113.5	7.1	629	2	A46500	Ly-9.2 antigen - m	343	104	6.5	802	1	TVHUP4	fibroblast growth
271	113.5	7.1	647	2	B41288	vascular cell adhe	344	103.5	6.4	588	2	JH0506	adhesion molecule
272	113.5	7.1	748	2	S41050	fibroblast growth	345	103.5	6.4	588	2	A45254	surface glycoprote
273	113.5	7.1	806	2	A35963	protein-tyrosine k	346	103.5	6.4	818	2	JC4058	fibroblast growth
274	113.5	7.1	976	1	TVMSMD	macrophage colony	347	103	6.4	309	2	S15674	cell surface glyco
275	113.5	7.1	1021	2	A57112	contactin precurs	348	103	6.4	650	1	JC1450	fibroblast growth
276	113	7.0	626	1	A61084	myelin-associated	349	103	6.4	1666	2	A48594	skelemin - mouse
277	113	7.0	705	2	S51635	fibroblast growth	350	103	6.4	2295	2	C88369	protein unc-52 [1m
278	113	7.0	1173	2	T25893	hypothetical prote	351	103	6.4	3375	2	T19821	hypothetical prote
279	113	7.0	1259	2	S36126	neural cell adhesi	352	102.5	6.4	255	2	JC7593	SH2 domain-contain
280	112.5	7.0	288	2	A45803	B-cell-restricted	353	102.5	6.4	278	2	JC1507	biliary glycoprote
281	112.5	7.0	733	2	I49293	fibroblast growth	354	102.5	6.4	508	2	A33378	fasciclin III prec
282	112.5	7.0	1020	2	S05944	neural cell surf	355	102.5	6.4	1176	2	JN0583	myosin-light-chain
283	112.5	7.0	1138	2	S24614	myosin-binding pro	356	102	6.4	336	2	C27658	pregnancy-specific
284	112	7.0	503	2	JC5287	SHP substrate-1 pr	357	102	6.4	362	2	A45897	MHC class I histoc
285	112	7.0	1209	2	T42718	probable neural ce	358	102	6.4	398	2	A39371	Ig V-region-like B
286	111.5	6.9	413	2	A37778	hemolin precursor	359	102	6.4	416	1	A42879	advanced glycosyla
287	111.5	6.9	584	2	I50419	s-glycerin precurs	360	102	6.4	530	2	A53437	poliovirus recepto
288	111.5	6.9	978	2	S16385	macrophage colony	361	102	6.4	640	2	A43273	herregulin precurs
289	111	6.9	613	4	C40201	artifactor-warnin s	362	101.5	6.3	270	2	S65739	basigin precursor
290	110.5	6.9	341	2	JC1511	biliary glycoprote	363	101.5	6.3	523	2	I50478	neutrolin - goldfis
291	110.5	6.9	344	1	RWRTC2	T-cell surface gly	364	101.5	6.3	1000	2	I46521	titin - rabbit (fr
292	110.5	6.9	588	2	I37202	B-CAM protein - hu	365	101.5	6.3	1089	1	S33727	platelet-derived g
293	110.5	6.9	729	2	A56795	fibroblast growth	366	101	6.3	462	2	I38404	neu differentiatio
294	110	6.9	238	2	S31779	trypsin (EC 3.4.21	367	101	6.3	627	4	A40201	artifactor-warnin s
295	110	6.9	639	2	I61719	neu differentiatio	368	100.5	6.3	372	2	C39371	Ig V-region-like B
296	110	6.9	822	2	B49151	fibroblast growth	369	100.5	6.3	817	2	A48721	titin, muscle - ch
297	109.5	6.8	495	2	T25750	hypothetical prote	370	100	6.2	264	2	T26976	hypothetical prote
298	109.5	6.8	822	2	S19947	fibroblast growth	371	100	6.2	277	2	I52825	gene MAC25 protein
299	109.5	6.8	1021	2	T42634	connectin/titin -	372	100	6.2	282	2	JH0291	class I histocompa
300	109.5	6.8	1040	2	A57638	receptor tyrosine	373	100	6.2	362	2	JH0291	butyrophilin precu
301	109.5	6.8	1103	2	T22889	hypothetical prote	374	100	6.2	526	2	S70587	protein-tyrosine k
302	109	6.8	520	1	S44099	brain-derived neur	375	100	6.2	974	1	A49714	protein C18F3.3 [i
303	109	6.8	582	1	BNRT3S	myelin-associated	376	99.5	6.2	304	2	B88746	prostatoclin-stimu
304	109	6.8	626	1	BNRT3S	myelin-associated	377	99.5	6.2	309	2	T15747	hypothetical prote
305	109	6.8	637	2	B33785	myelin-associated	378	99.5	6.2	612	2	I73633	gene trkC protein
306	109	6.8	818	1	S44098	brain-derived neur	379	99.5	6.2	825	2	A55178	neutrophilin recep
307	109	6.8	1272	2	S26180	neurofascin - chic	380	99.5	6.2	839	1	I73632	neutrophilin-3 rec
308	109	6.8	1880	2	T18531	tractin - mediana	381	99.5	6.2	1287	2	T30988	hypothetical prote
309	108.5	6.8	339	2	T28138	Ig V-region-like B	382	99	6.2	475	2	I76668	pregnancy-specific
310	108.5	6.8	404	1	I61596	advanced glycosyla	383	99	6.2	874	2	T29548	hypothetical prote
311	108.5	6.8	487	2	S65133	butyrophilin - mou	384	98.5	6.1	268	2	T23555	hypothetical prote
312	108	6.7	340	2	T28137	Ig V-region-like B	385	98.5	6.1	422	2	S32357	glial growth facto
313	108	6.7	799	1	TVRTTB	nerve growth facto	386	98.5	6.1	738	2	A40096	platelet-endothell
314	107.5	6.7	637	2	C43273	herregulin precurs	387	98.5	6.1	1327	2	T09402	immunoglobulin-lik
315	107.5	6.7	662	2	I61722	neu differentiatio	388	98.5	6.1	1462	1	B36182	protein-tyrosine-p
316	107.5	6.7	750	2	S41051	fibroblast growth	389	98	6.1	240	2	JL0143	antigen BCM1 precu
317	107	6.7	267	2	A38442	probable tumor sup	390	98	6.1	356	2	JH0289	class I histocompa
318	107	6.7	599	2	T16774	hypothetical prote	391	98	6.1	583	2	I39428	alcan - human
319	107	6.7	820	2	T17295	fibroblast growth	392	98	6.1	1052	2	A49120	protein-tyrosine k
320	106.5	6.6	289	2	G00031	B7 protein - red-c	393	98	6.1	1088	1	PPRTGA	platelet-derived g
321	106.5	6.6	391	2	T09058	butyrophilin homol	394	98	6.1	1142	2	S36845	myosin-binding pro

395	98	6.1	1191	2	S35305	zinc finger protei	468	89.5	5.6	354	1	LKHU	proteoglycan link
396	97.5	6.1	421	2	T46266	hypothetical prote	469	89.5	5.6	618	2	T08685	hypothetical prote
397	97.5	6.1	960	1	JN0677	protein-tyrosine k	470	89	5.5	219	2	PC4203	Ig kappa chain (mo
398	97.5	6.1	1451	2	S42167	190K protein - hum	471	89	5.5	230	2	A56210	neu differentiatio
399	97	6.0	362	2	JH0292	class I histocompa	472	89	5.5	264	2	I46020	FC gamma 2 recepto
400	97	6.0	978	1	A49814	protein-tyrosine k	473	89	5.5	339	2	JC7509	glycoprotein Vi-1
401	97	6.0	1147	2	A59307	myosin-light-chain	474	89	5.5	347	2	S41638	T-cell surface gly
402	96.5	6.0	370	2	S29139	aggreca - pig (fr	475	89	5.5	362	2	JH0288	class I histocompa
403	96.5	6.0	1244	2	T49632	hypothetical prote	476	89	5.5	510	2	PC4054	cardiac C-protein
404	96	6.0	304	1	RWCHH7	cell surface glyco	477	89	5.5	980	1	TVCTMD	macrophage colony-
405	96	6.0	687	2	A49636	soluble vascular e	478	88.5	5.5	348	2	I68745	MHC class I lympho
406	96	6.0	713	2	I50128	fibroblast growth	479	88.5	5.5	1021	2	I39207	leukocyte surface
407	96	6.0	839	2	JC4583	fibroblast growth	480	88.5	5.5	1592	2	T16055	hypothetical prote
408	96	6.0	894	1	A41527	protein-tyrosine k	481	88.5	5.5	1723	2	H85557	polymorphic membra
409	96	6.0	999	2	I38547	novel cellular pro	482	88.5	5.5	1723	2	E72067	polymorphic membra
410	95.5	6.0	240	2	JC4121	pregnancy-specific	483	88.5	5.5	1732	2	C81601	class I histocompa
411	95.5	6.0	269	2	A46506	leukocyte activati	484	88	5.5	255	1	S48146	muscln I precursor,
412	95.5	6.0	1132	2	A35089	myosin-binding pro	485	88	5.5	362	2	JH0290	class I histocompa
413	95	5.9	167	2	S29579	Ig light chain - r	486	88	5.5	790	2	A39627	protein-tyrosine k
414	95	5.9	219	2	S52028	Ig kappa chain - m	487	87.5	5.5	666	2	I58169	semaphorin III - m
415	95	5.9	241	2	D43273	heregulin precurs	488	87	5.4	238	2	A49633	Ig lambda-like cha
416	95	5.9	749	2	G01856	semaphorin V - hum	489	87	5.4	313	2	H36854	hemagglutinin - va
417	94.5	5.9	273	2	JX0107	basigin precursor	490	87	5.4	330	2	I46691	CD86 precursor - r
418	94.5	5.9	321	2	I54766	B-lymphocyte activ	491	87	5.4	342	2	S33355	class I histocompa
419	94.5	5.9	825	1	A40026	neutrophin-3 rec	492	87	5.4	408	1	LKXT2	proteoglycan link
420	94.5	5.9	890	1	A53743	protein-tyrosine k	493	86.5	5.4	116	2	S20708	Ig kappa chain V r
421	94	5.9	241	2	S32359	glial growth facto	494	86.5	5.4	172	2	B26414	95K nonspecific cr
422	94	5.9	288	2	B45897	MHC class I histoc	495	86.5	5.4	210	2	F82238	phosphoribosyl-AMP
423	94	5.9	697	2	T34006	hypothetical prote	496	86.5	5.4	270	2	A34636	FC-gamma receptor
424	94	5.9	702	2	T21148	hypothetical prote	497	86.5	5.4	274	2	T32736	hypothetical prote
425	94	5.9	1679	2	T30271	surface protein -	498	86.5	5.4	285	2	S36903	FC gamma (IgG) rec
426	93.5	5.8	287	2	PS0401	basigin type II -	499	86.5	5.4	375	2	I60125	PDGF receptor beta
427	93.5	5.8	271	2	S43512	GP42/Basigin prote	500	86.5	5.4	707	2	JC7763	neutroal leucine-r
428	93.5	5.8	275	2	PS0402	basigin type III -	501	86	5.4	220	2	A49444	Ig gamma-1 heavy c
429	93.5	5.8	345	2	A46052	vascular cell adhe	502	86	5.4	243	2	A37982	calcium vector pro
430	93.5	5.8	592	2	S25705	Ig mu chain - shee	503	86	5.4	395	2	T31822	hypothetical prote
431	93.5	5.8	729	2	A49120	fibroblast growth	504	86	5.4	478	2	I53960	PRR2 alpha - human
432	93.5	5.8	876	2	I49152	protein-tyrosine k	505	86	5.4	562	2	G02426	interleukin-1 rece
433	93.5	5.8	880	2	B53743	protein-tyrosine k	506	86	5.4	880	1	JC4166	protein-tyrosine k
434	93.5	5.8	1437	2	T31093	probable protein-t	507	86	5.4	954	2	H97100	DNA gyrase A chain
435	93	5.8	524	2	D82944	platelet-derived g	508	86	5.4	964	2	T15746	hypothetical prote
436	93	5.8	1089	1	PFHUGA	Ig kappa chain (Wa	509	85.5	5.3	283	1	FCMSG1	FC gamma (IgG) rec
437	92.5	5.8	214	2	S68212	proteoglycan link	510	85.5	5.3	302	2	C36464	fibroblast growth
438	92.5	5.8	354	1	S04243	neutrophin-3 rec	511	85.5	5.3	341	2	I51158	major histocompati
439	92.5	5.8	525	1	A58674	neutrophin-3 rec	512	85.5	5.3	369	2	AB2550	hypothetical prote
440	92.5	5.8	803	1	S35695	hypothetical prote	513	85.5	5.3	558	2	JC5204	60K cysteine-rich
441	92.5	5.8	818	2	T19120	hypothetical prote	514	85.5	5.3	619	2	S45932	tyrosine transport
442	92.5	5.8	852	2	I51259	tyrosine kinase C	515	85.5	5.3	625	2	T16777	hypothetical prote
443	92.5	5.8	882	2	I38912	receptor tyrosine	516	85.5	5.3	1398	2	T25568	hypothetical prote
444	92.5	5.8	2109	2	E89066	protein H05009.1 [517	85.5	5.3	1748	1	JN0786	integrin beta-4 ch
445	92.5	5.8	2109	2	T33247	hypothetical prote	518	85.5	5.3	2415	1	A39086	aggreca precursor
446	92.5	5.8	2179	1	GNNYH4	genome polypeptid	519	85	5.3	207	2	A56190	titin - rat (fragm
447	92.5	5.8	2541	2	T29340	hypothetical prote	520	85	5.3	217	2	S42772	Ig kappa chain - m
448	92	5.7	370	2	C71926	cag island protein	521	85	5.3	330	2	A40071	FC gamma (IgG) rec
449	91.5	5.7	329	2	A40730	class I histocompa	522	85	5.3	330	2	I49660	FC-gamma-1/gamma-2
450	91.5	5.7	402	2	T09062	probable advanced	523	85	5.3	362	2	A45849	MHC class I histoc
451	91.5	5.7	1465	2	S34529	165K protein, skel	524	85	5.3	416	2	S33473	interleukin-1 rece
452	91	5.7	265	2	C39797	DM-GRASP precursor	525	85	5.3	528	2	T50012	hypothetical prote
453	91	5.7	587	2	JH0464	MHC class II histo	526	85	5.3	2013	2	AD1129	probable peptidogl
454	91	5.7	975	1	TVMSKT	protein-tyrosine k	527	84.5	5.3	257	2	S00682	IgG FC receptor al
455	91	5.7	994	2	I49276	c-met tyrosine kin	528	84.5	5.3	532	1	A29849	intercellular adhe
456	90.5	5.6	354	1	S42938	proteoglycan link	529	84.5	5.3	547	1	S28904	carcinomembryonic
457	90.5	5.6	832	2	AD1096	interleukin-1 rece	530	84.5	5.3	709	2	A35364	killer cell inhibi
458	90.5	5.6	937	2	A45082	neutrotrophic recep	531	84.5	5.3	841	2	JC5894	hypothetical prote
459	90.5	5.6	1060	2	S63252	hypothetical prote	532	84.5	5.3	876	2	G90592	desmocollin - bovi
460	90.5	5.6	1214	2	A28452	proteoglycan core	533	84.5	5.3	896	2	I45858	Ig heavy chain - c
461	90.5	5.6	2132	1	A55182	aggreca precursor	534	84.5	5.3	1005	2	T18537	Ig heavy chain - c
462	90	5.6	340	2	JC7505	brain link protein	535	84.5	5.3	1452	1	S17669	protein-tyrosine-p
463	90	5.6	401	2	E83720	methyl-accepting c	536	84.5	5.3	1452	1	S17670	protein-tyrosine-p
464	90	5.6	666	2	H89581	protein dim-1 [imp	537	84.5	5.3	1778	2	AF1116	internalin protein
465	90	5.6	1643	2	T14274	versican precursor	538	84.5	5.3	2109	1	I50421	aggreca precursor
466	90	5.6	3381	2	T42389	versican precursor	539	84	5.2	210	2	AH1039	phage repressor pr
467	89.5	5.6	188	2	E87048	probable lipoprote	540	84	5.2	225	2	JL0029	Ig kappa chain pre

541	84	5.2	275	1	HLHU10	MHC class I histoc	614	80.5	5.0	366	2	I72113	MHC histocompatibi
542	84	5.2	313	2	JQ1862	31R protein - vari	615	80.5	5.0	366	2	I38507	MHC class I histoc
543	84	5.2	362	2	A45845	MHC class I histoc	616	80.5	5.0	613	2	T27528	hypothetical prote
544	84	5.2	380	2	S12839	Ig heavy chain pre	617	80.5	5.0	905	2	T38944	probable coatome
545	84	5.2	458	1	RWHU74	T-cell surface gly	618	80.5	5.0	547	1	IJFETM	cadherin-related t
546	84	5.2	1185	2	T46428	hypothetical prote	619	80.5	5.0	13055	2	T16580	hypothetical prote
547	84	5.2	1537	2	S53465	floculation prote	620	80	5.0	125	2	S62676	hergulin isoform
548	83.5	5.2	221	2	A82190	hypothetical prote	621	80	5.0	215	2	JB0243	Ig kappa chain NIG
549	83.5	5.2	229	2	A20969	Ig kappa chain pre	622	80	5.0	247	1	A54662	myelin P0 protein
550	83.5	5.2	238	2	I68699	MHC HLA-A cell sur	623	80	5.0	283	1	LNPHLS	lectin precursor -
551	83.5	5.2	355	2	B40730	class I histocompa	624	80	5.0	292	1	KFRB3	tissue factor prec
552	83.5	5.2	358	2	A28834	MHC class I histoc	625	80	5.0	325	2	I54449	MHC class I HLA-Cx
553	83.5	5.2	388	2	AF1383	internalin protein	626	80	5.0	355	2	B26883	neural cell adhesi
554	83.5	5.2	398	2	S17428	interleukin-1 rece	627	80	5.0	363	1	S42102	MHC class I histoc
555	83.5	5.2	411	1	D64079	probable N-carbamyl	628	80	5.0	365	1	HLHUA2	MHC class I histoc
556	83.5	5.2	684	2	S60266	novel antigen rece	629	80	5.0	365	2	I37470	HLA-A*0210 - human
557	83.5	5.2	755	2	T03219	G-quartet DNA bind	630	80	5.0	365	2	I84448	MHC class I histoc
558	83.5	5.2	941	1	TVWMD	protein-tyrosine k	631	80	5.0	365	2	I61857	MHC HLA-A2.4a chai
559	83.5	5.2	4436	2	E71086	hypothetical prote	632	80	5.0	399	1	G2MSAM	Ig gamma-2a chain
560	83	5.2	175	2	A39171	T-cell surface gly	633	80	5.0	454	2	F90602	aminopeptidase (le
561	83	5.2	197	2	PQ0327	heparin-binding fi	634	80	5.0	457	2	A27449	T-cell surface gly
562	83	5.2	240	2	A39016	T-cell surface gly	635	80	5.0	473	2	G95963	pyruvate kinase (p
563	83	5.2	365	2	I38443	gene HLA-A-0203 pr	636	80	5.0	487	2	T28804	hypothetical prote
564	83	5.2	3507	2	T34513	hypothetical prote	637	80	5.0	575	2	F88369	protein T7N9.26 [i
565	82.5	5.1	230	2	S33161	Ig kappa chain - s	638	80	5.0	643	2	F84117	hypothetical prote
566	82.5	5.1	351	1	RWHUC2	T-cell surface gly	639	80	5.0	701	2	T19605	hypothetical prote
567	82.5	5.1	439	2	AE1251	probable peptidogl	640	80	5.0	718	2	AB1258	hypothetical prote
568	82.5	5.1	513	2	A71004	hypothetical prote	641	80	5.0	1123	2	T47687	adaptor protein/ a
569	82.5	5.1	987	2	A88746	protein C18R3.2 [i	642	80	5.0	1160	2	F88369	protein unc-52 [im
570	82.5	5.1	1330	2	A36373	hypothetical prote	643	80	5.0	1578	2	AD1512	peptidoglycan boun
571	82.5	5.1	2327	2	T42630	aggreccan - bovine	644	80	5.0	1871	2	D96698	probable DNA polym
572	82	5.1	194	2	T29925	hypothetical prote	645	80	5.0	1894	2	T02155	DNA-directed DNA p
573	82	5.1	205	2	A48929	activated B-cell p	646	80	5.0	1983	2	G86643	hypothetical prote
574	82	5.1	253	2	T15475	hypothetical prote	647	79.5	5.0	234	2	S01320	Ig kappa chain pre
575	82	5.1	267	2	B71062	hypothetical prote	648	79.5	5.0	295	1	KFRU03	tissue factor prec
576	82	5.1	313	2	T28598	hypothetical prote	649	79.5	5.0	323	2	A48997	tumor surface anti
577	82	5.1	352	2	I51541	MHC class I antige	650	79.5	5.0	365	2	A47636	MHC class I histoc
578	82	5.1	356	2	A27797	class I histocompa	651	79.5	5.0	366	2	A52823	MHC class I histoc
579	82	5.1	365	2	I61902	MHC class I histoc	652	79.5	5.0	381	2	I51174	Ig heavy chain - R
580	82	5.1	365	2	I38441	gene HLA-A-6802 pr	653	79.5	5.0	416	2	A54017	colon carcinoma-as
581	82	5.1	365	2	I38442	gene HLA-A-0205 pr	654	79.5	5.0	475	2	A54879	pregnancy-specific
582	82	5.1	370	2	B64587	cag pathogenicity	655	79.5	5.0	568	2	A45804	Ig mu chain C regi
583	82	5.1	411	2	A81336	probable fibronect	656	79.5	5.0	605	2	S67815	protein-tyrosine k
584	82	5.1	680	2	JCS595	killer cell inhibi	657	79.5	5.0	772	2	I48747	semaphorin D - mou
585	82	5.1	938	2	T01809	hypothetical prote	658	79.5	5.0	811	2	PN0689	connectin I - chic
586	82	5.1	1213	2	T19835	hypothetical prote	659	79.5	5.0	830	2	T43999	glycoprotein B [im
587	82	5.1	1256	2	G97902	alpha-amylase (EC	660	79.5	5.0	971	2	G75503	hypothetical prote
588	81.5	5.1	210	2	A56169	Ig kappa chain V r	661	79.5	5.0	972	1	TVHUMD	macrophage colony-
589	81.5	5.1	224	2	I37243	CWRF-35 antigen -	662	79.5	5.0	977	2	I45877	protein-tyrosine k
590	81.5	5.1	233	2	JH0372	42K surface glycop	663	79.5	5.0	1104	2	C72409	reverse gyrase - T
591	81.5	5.1	316	2	D71535	probable NADH (ubi	664	79.5	5.0	1385	2	D89824	hypothetical prote
592	81.5	5.1	355	2	I80169	class I histocompa	665	79.5	5.0	2314	1	A46151	protein-tyrosine-p
593	81.5	5.1	537	2	A54000	surface protein T6	666	79	4.9	135	2	S40342	Ig kappa chain - h
594	81.5	5.1	635	2	JCS596	killer cell inhibi	667	79	4.9	182	2	A25468	T-cell surface gly
595	81.5	5.1	1335	2	T17508	glycoprotein Vp260	668	79	4.9	313	2	B70755	probable lprB prot
596	81	5.0	164	2	T19795	hypothetical prote	669	79	4.9	385	2	I36958	MHC ChLA chain - c
597	81	5.0	196	2	T19794	hypothetical prote	670	79	4.9	357	2	I67482	MHC class I heavy
598	81	5.0	276	2	S20690	31.6K hypothetical	671	79	4.9	405	1	G2MSBM	Ig gamma-2b chain
599	81	5.0	290	2	AG2216	hypothetical prote	672	79	4.9	407	2	T08732	hypothetical prote
600	81	5.0	362	2	JH0541	class I histocompa	673	79	4.9	468	2	T40223	HMG-box containing
601	81	5.0	362	2	JH0539	class I histocompa	674	79	4.9	481	2	S26698	alkaline proteinase
602	81	5.0	362	2	JH0540	class I histocompa	675	79	4.9	556	1	I32602	60K cysteine-rich
603	81	5.0	1087	2	I51552	platelet-derived g	676	79	4.9	556	2	A86560	phosphoglucosidase
604	81	5.0	1286	2	T16507	hypothetical prote	677	79	4.9	582	2	B86366	probable cell surf
605	80.5	5.0	119	2	B27588	Ig kappa chain pre	678	79	4.9	657	2	AD1525	semaphorin III pre
606	80.5	5.0	178	2	PT0219	Ig kappa chain V-C	679	79	4.9	771	2	D49423	iron(III) dicitrat
607	80.5	5.0	266	2	A28031	MHC class II histo	680	79	4.9	774	1	QRECPA	alpha-1 proteinase
608	80.5	5.0	329	1	A48754	B7-2 antigen - hum	681	79	4.9	785	2	A29953	myosin-light-chain
609	80.5	5.0	335	2	S58892	signaling lymphocy	682	79	4.9	815	2	JG0197	receptor-like prot
610	80.5	5.0	345	2	I68749	MHC class I lympho	683	79	4.9	871	2	T45692	hypothetical prote
611	80.5	5.0	357	2	I36965	MHC class I protei	684	79	4.9	1014	2	T13476	hypothetical prote
612	80.5	5.0	365	2	S01171	class I histocompa	685	79	4.9	1073	2	T33764	hypothetical prote
613	80.5	5.0	366	2	I37526	MHC class I histoc	686	79	4.9	1684	2	S10789	amylase A-180 - al

687	79	4.9	1922	2	T00637	hypothetical prote	760	77.5	4.8	5291	2	F90696	hypothetical prote
688	78.5	4.9	237	2	G28043	MHC class II histo	761	77	4.8	219	2	S16112	Ig kappa chain V r
689	78.5	4.9	254	1	JL0107	Fc gamma (IgG) rec	762	77	4.8	265	2	B90242	conserved hypotet
690	78.5	4.9	261	2	E39797	MHC class II DR-be	763	77	4.8	289	2	B86794	hypothetical prote
691	78.5	4.9	318	2	F72171	K9R protein - vari	764	77	4.8	328	2	I47160	Ig gamma 2b chain
692	78.5	4.9	348	2	S09273	Ig alpha chain C r	765	77	4.8	328	2	I47159	Ig gamma 2a chain
693	78.5	4.9	357	2	I36966	MHC class I protei	766	77	4.8	329	2	A44065	fibroblast growth
694	78.5	4.9	365	2	JH0535	class I histocompa	767	77	4.8	339	2	A45071	MHC class I histoc
695	78.5	4.9	365	2	I83063	All.2 - human	768	77	4.8	355	1	LKCH	proteoglycan link
696	78.5	4.9	366	2	I37527	MHC class I histoc	769	77	4.8	365	2	I37542	MHC class I histoc
697	78.5	4.9	368	2	T24408	hypothetical prote	770	77	4.8	366	2	I81232	lymphocyte antigen
698	78.5	4.9	393	1	GLMSM	Ig gamma-1 chain C	771	77	4.8	366	2	I37135	MHC class I histoc
699	78.5	4.9	403	2	I52590	m33-B isoform - mo	772	77	4.8	370	1	HLAUA3	MHC class I histoc
700	78.5	4.9	432	2	D83904	carbon storage regu	773	77	4.8	423	2	T23223	hypothetical prote
701	78.5	4.9	457	2	H85013	hypothetical prote	774	77	4.8	462	1	A37986	interleukin-6 rece
702	78.5	4.9	480	2	T04849	protein kinase hom	775	77	4.8	549	2	S04845	Ig heavy chain pre
703	78.5	4.9	545	2	JU0341	intercellular adhe	776	77	4.8	658	2	S69418	protein phosphatas
704	78.5	4.9	628	2	P84219	Htr16 transducer l	777	77	4.8	656	2	S01283	hypothetical prote
705	78.5	4.9	718	2	AF1620	hypothetical prote	778	77	4.8	790	1	TVHUTT	nerve growth facto
706	78.5	4.9	943	2	B45082	neurotrophic recep	779	77	4.8	1298	2	A64157	hypothetical prote
707	78.5	4.9	1036	2	B69368	hypothetical prote	780	77	4.8	1819	2	T32008	hypothetical prote
708	78.5	4.9	1183	2	S63046	probable membrane	781	77	4.8	1848	2	A44140	cellulose-binding
709	78.5	4.9	1280	2	E95031	alkaline amylopull	782	76.5	4.8	113	1	KVMS17	Ig kappa chain V r
710	78.5	4.9	1734	2	A41101	phorbol ester-bind	783	76.5	4.8	237	2	I54294	MHC HLA-DR-beta su
711	78.5	4.9	1742	2	S24600	projectin - fruit	784	76.5	4.8	246	2	A47712	myelin/oligodendro
712	78.5	4.9	1813	2	T19295	hypothetical prote	785	76.5	4.8	266	2	A42621	MHC class II histo
713	78	4.9	218	2	S22131	sucrose synthase (786	76.5	4.8	281	2	S00853	probable major tai
714	78	4.9	237	2	G60497	H-2 class II histo	787	76.5	4.8	363	2	S07113	class I histocompa
715	78	4.9	248	1	MPRT0	myelin P0 protein	788	76.5	4.8	365	2	I84432	MHC class I protei
716	78	4.9	256	2	T24711	hypothetical prote	789	76.5	4.8	365	2	JL0135	MHC class I histoc
717	78	4.9	296	2	I46021	Fc-gamma receptor	790	76.5	4.8	366	2	B37028	MHC class I histoc
718	78	4.9	316	2	C37028	MHC class I histoc	791	76.5	4.8	379	2	E96842	hypothetical prote
719	78	4.9	342	2	T33768	hypothetical prote	792	76.5	4.8	406	2	D90492	hypothetical prote
720	78	4.9	362	2	C40730	class I histocompa	793	76.5	4.8	612	2	S33506	protein-tyrosine k
721	78	4.9	365	2	I36961	MHC class I protei	794	76.5	4.8	625	2	D87793	protein C27A12.2 l
722	78	4.9	366	2	T27949	hypothetical prote	795	76.5	4.8	772	2	A49069	collapsin - chicke
723	78	4.9	366	2	I37544	MHC class I histoc	796	76.5	4.8	830	1	B44047	glycoprotein B pre
724	78	4.9	366	2	I37523	MHC class I histoc	797	76.5	4.8	830	2	T44186	probable glycoprot
725	78	4.9	403	2	B88633	protein F56B3.9 f	798	76.5	4.8	831	1	VGBE68	glycoprotein B - h
726	78	4.9	440	2	JL0144	interleukin-6 rece	799	76.5	4.8	891	2	H36790	hypothetical prote
727	78	4.9	460	2	JL0145	interleukin-6 rece	800	76.5	4.8	1152	2	AC1347	probable peptidogl
728	78	4.9	468	2	A41518	transcription fact	801	76.5	4.8	1611	1	WMTMPV	183K protein - pep
729	78	4.9	537	2	A46611	myosin-binding pro	802	76.5	4.8	2871	2	A55624	fibrillin-1 precur
730	78	4.9	556	2	A44441	B-cell antigen CD1	803	76.5	4.8	5188	2	B85547	probable RXR famil
731	78	4.9	611	2	AB1497	internalin protein	804	76	4.7	171	1	RWHUD1	T-cell surface gly
732	78	4.9	621	2	JQ1685	anthranilate synth	805	76	4.7	265	2	B39797	MHC class II histo
733	78	4.9	621	2	S27752	anthranilate synth	806	76	4.7	274	2	A47639	OX-2 membrane glyc
734	78	4.9	717	2	T29816	hypothetical prote	807	76	4.7	277	2	I47162	Ig gamma 4 chain c
735	78	4.9	782	2	T43277	host cell factor 1	808	76	4.7	326	1	WMV215	B15R protein precu
736	78	4.9	931	2	T33744	hypothetical prote	809	76	4.7	326	2	T37450	interleukin-1 beta
737	78	4.9	953	2	T08961	hypothetical prote	810	76	4.7	349	2	JC6311	interferon recepto
738	78	4.9	954	2	E86174	protein F19P19.26	811	76	4.7	359	1	HLHU12	MHC class I histoc
739	78	4.9	1267	1	MXR32	lambda 3 protein -	812	76	4.7	400	2	AD2260	hypothetical prote
740	77.5	4.8	160	2	I47163	cytolytic trigger	813	76	4.7	406	2	A35360	otefin - fruit fly
741	77.5	4.8	229	1	TRB0TR	trypsin (EC 3.4.21	814	76	4.7	462	2	F83510	flagellar hook pro
742	77.5	4.8	235	2	I68700	MHC HLA-A cell sur	815	76	4.7	476	2	A71302	conserved hypotet
743	77.5	4.8	238	2	I71907	MHC H2-IE-beta cel	816	76	4.7	477	2	S50738	Qcr1 protein - yea
744	77.5	4.8	264	2	S10989	class II histocomp	817	76	4.7	486	2	D64474	hypothetical prote
745	77.5	4.8	266	2	D39797	MHC class II histo	818	76	4.7	498	2	S11246	LAG-3 protein prec
746	77.5	4.8	266	2	A25324	class II histocomp	819	76	4.7	521	2	I39956	neutral proteinase
747	77.5	4.8	266	2	I54448	MHC class II histo	820	76	4.7	569	2	A36187	interleukin-1 rece
748	77.5	4.8	338	2	A39953	MHC class I histoc	821	76	4.7	569	2	A46462	T cell activation
749	77.5	4.8	339	2	A37028	MHC class I histoc	822	76	4.7	834	2	A97178	probable pamease
750	77.5	4.8	365	2	JH0534	class I histocompa	823	76	4.7	856	2	I58411	protein-tyrosine k
751	77.5	4.8	365	2	I37477	MHC class I histoc	824	76	4.7	878	2	T08559	protein kinase hom
752	77.5	4.8	377	2	T05354	hypothetical prote	825	76	4.7	990	2	E90433	conserved hypotet
753	77.5	4.8	428	2	A82215	probable alanine r	826	76	4.7	1003	2	T13856	ksr protein - frui
754	77.5	4.8	544	2	JC5018	intercellular adhe	827	76	4.7	1054	2	T39333	protein phosphatas
755	77.5	4.8	573	2	T09940	calcium-dependent	828	76	4.7	1157	2	T40572	hypothetical prote
756	77.5	4.8	694	2	I40866	exo-alpha-sialidas	829	76	4.7	1177	2	T16594	lambda 3 protein -
757	77.5	4.8	1315	2	T28679	fibrinogen-binding	830	76	4.7	1267	1	MXR31	genome polypeptide
758	77.5	4.8	1797	2	F69195	cell surface glyco	831	76	4.7	2185	1	JQ2021	hypothetical prote
759	77.5	4.8	2044	2	AB1180	probable peptidogl	832	76	4.7	2271	2	F90073	

833 75.5 4.7 109 2 PH0091 Ig kappa chain V r
834 75.5 4.7 113 2 PU0203 anti-DNA autoantib
835 75.5 4.7 233 1 JU0284 PC gamma (IgG) rec
836 75.5 4.7 238 2 A53278 MHC class II histo
837 75.5 4.7 251 2 I38053 myelin protein zer
838 75.5 4.7 266 2 I54295 lymphocyte antigen
839 75.5 4.7 340 2 S11143 class I histocompa
840 75.5 4.7 357 2 S18198 class I histocompa
841 75.5 4.7 358 2 S09268 Ig alpha chain C r
842 75.5 4.7 365 2 JH0536 class I histocompa
843 75.5 4.7 365 2 I37483 HLA-Aw34.2 antigen
844 75.5 4.7 365 2 I38610 MHC class I histoc
845 75.5 4.7 366 2 JH0536 MHC class I histoc
846 75.5 4.7 393 2 C71254 hypohetical prote
847 75.5 4.7 412 2 B44418 surface antigen -
848 75.5 4.7 503 2 S63257 probable membrane
849 75.5 4.7 546 2 I48899 cortactin - mouse
850 75.5 4.7 566 2 C81870 probable single-st
851 75.5 4.7 610 2 AB1472 two-component sens
852 75.5 4.7 621 2 AC1974 hypohetical prote
853 75.5 4.7 646 1 S15901 chromogranin B pre
854 75.5 4.7 874 2 B86322 FGA14.8 protein -
855 75.5 4.7 891 2 T40137 hypohetical serin
856 75.5 4.7 1016 2 T00375 hypohetical prote
857 75.5 4.7 1133 1 EGRT epidermal growth f
858 75.5 4.7 1289 2 T72308 hypohetical prote
859 75.5 4.7 4717 2 T41581 hypohetical coile
860 75 4.7 219 2 S38855 Ig kappa chain - m
861 75 4.7 248 1 JH0252 myelin P0 protein
862 75 4.7 306 2 T24589 hypohetical prote
863 75 4.7 322 1 TVB922 GTP-binding protei
864 75 4.7 322 2 A75067 abc transporter, p
865 75 4.7 325 2 H07822 probable ompA prot
866 75 4.7 353 2 G02922 MHC class I lero-G
867 75 4.7 365 2 I37478 MHC class I histoc
868 75 4.7 366 2 I59622 lymphocyte antigen
869 75 4.7 398 2 I49433 gene 2B4 protein -
870 75 4.7 474 1 OMHUIB alpha-1-B-glycopro
871 75 4.7 507 1 A43387 polymerase-asecia
872 75 4.7 507 2 S33192 phase-1 flagellin
873 75 4.7 507 2 JQ1929 phosphoprotein - r
874 75 4.7 508 2 A53465 phase I flagellin
875 75 4.7 544 1 A48961 beta-amylase - Bac
876 75 4.7 551 2 G84301 hypohetical prote
877 75 4.7 620 2 AG1598 internalin like pr
878 75 4.7 648 2 H08898 envelope-like - so
879 75 4.7 678 2 H82379 methyl-accepting c
880 75 4.7 748 2 I48744 semaphorin A - mou
881 75 4.7 755 2 H86561 C7456 hypohetical
882 75 4.7 755 2 B72061 hypohetical prote
883 75 4.7 854 2 S13288 env protein - huma
884 75 4.7 875 2 H90371 proteinase [import
885 75 4.7 1055 2 AD2499 hypohetical prote
886 75 4.7 1065 2 S19482 hypohetical prote
887 75 4.7 1104 2 S59310 probable membrane
888 75 4.7 1124 2 T30340 daRNA adenosine de
889 75 4.7 1176 2 A33856 surface-layer 125K
890 75 4.7 2175 1 GNNYBE genome polyprotein
891 75 4.7 2185 1 GNNYBT genome polyprotein
892 75 4.7 2193 2 S52919 polyprotein (IA, 1
893 75 4.7 5105 2 T32650 hypohetical prote
894 74.5 4.6 112 1 KVMSS1 Ig kappa chain V r
895 74.5 4.6 112 2 F27887 Ig kappa chain V r
896 74.5 4.6 131 2 B39276 Ig light chain pre
897 74.5 4.6 249 1 A61087 myelin P0 glycopro
898 74.5 4.6 264 2 I48432 MHC class II histo
899 74.5 4.6 266 2 B4261 MHC class II histo
900 74.5 4.6 266 2 B39260 MHC class II histo
901 74.5 4.6 321 2 D39371 Ig V-region-like B
902 74.5 4.6 328 2 S30444 SI2 protein - huma
903 74.5 4.6 344 2 B28967 T-cell surface gly
904 74.5 4.6 345 2 E71600 rifin PFB1040w - m
905 74.5 4.6 346 2 T35363 D-alanine-D-alanin

906 74.5 4.6 346 2 D97007 hypohetical prote
907 74.5 4.6 354 2 I54551 histocompatibility
908 74.5 4.6 354 2 I59308 class I histocompa
909 74.5 4.6 354 2 I80166 class I histocompa
910 74.5 4.6 354 2 I80167 class I histocompa
911 74.5 4.6 354 2 I80165 class I histocompa
912 74.5 4.6 354 2 I80168 class I histocompa
913 74.5 4.6 362 2 I61861 MHC HLA-B44.2 chai
914 74.5 4.6 362 2 I37519 MHC class I histoc
915 74.5 4.6 365 2 S16769 MHC class I histoc
916 74.5 4.6 365 2 JH0537 class I histocompa
917 74.5 4.6 365 2 I72170 MHC class I histoc
918 74.5 4.6 365 2 I38436 MHC class I histoc
919 74.5 4.6 365 2 I38519 MHC class I histoc
920 74.5 4.6 378 2 S61992 SIQ1 protein - yea
921 74.5 4.6 404 2 A46480 PC gamma (IgG) rec
922 74.5 4.6 409 1 G69000 molybdenum cofacto
923 74.5 4.6 432 1 RWMQ74 T-cell surface gly
924 74.5 4.6 504 2 S00390 Ig gamma chain (cl
925 74.5 4.6 524 2 A82580 polyvinylalcohol d
926 74.5 4.6 555 2 JQ1526 interleukin-1 rece
927 74.5 4.6 575 2 T33881 hypohetical prote
928 74.5 4.6 578 2 T33880 hypohetical prote
929 74.5 4.6 610 2 B84960 GTP-binding protei
930 74.5 4.6 706 2 A81848 probable TonB-depe
931 74.5 4.6 766 2 S37894 hypohetical prote
932 74.5 4.6 995 2 T27327 hypohetical prote
933 74.5 4.6 1016 2 T19006 ankyrin related pr
934 74.5 4.6 1052 2 T04439 hypohetical prote
935 74.5 4.6 1156 2 T23308 hypohetical prote
936 74.5 4.6 1507 2 T42631 breast cancer tumo
937 74.5 4.6 1807 2 JC6319 integrin beta-4 ch
938 74.5 4.6 3005 2 S33642 homeotic protein z
939 74 4.6 107 2 S57444 Ig kappa chain V-J
940 74 4.6 121 2 S40371 Ig kappa chain - h
941 74 4.6 135 2 B30563 T-cell receptor be
942 74 4.6 157 2 PH0201 hypohetical prote
943 74 4.6 215 2 JE0242 Ig kappa chain NIG
944 74 4.6 259 2 A98049 conserved hypotet
945 74 4.6 259 2 F95181 conserved hypotet
946 74 4.6 263 1 HLM8BU MHC class II histo
947 74 4.6 318 2 C81690 probable sodium-tr
948 74 4.6 344 2 A90040 hypohetical prote
949 74 4.6 359 2 I61867 MHC class I protei
950 74 4.6 368 2 A45831 MHC class I histoc
951 74 4.6 438 1 HVRK22 Ig mu chain C regi
952 74 4.6 437 2 T21716 hypohetical prote
953 74 4.6 455 2 AD1700 UDP-N-acetylmuramo
954 74 4.6 460 2 AB0656 hypohetical prote
955 74 4.6 476 2 A46118 myosin-binding pro
956 74 4.6 483 2 AH3445 GTP-binding protei
957 74 4.6 490 2 A35546 muscarinic acetyl
958 74 4.6 538 1 VGNZMM cell fusion glycop
959 74 4.6 570 2 A57535 intrileukin 1 recep
960 74 4.6 573 2 A86253 hypohetical prote
961 74 4.6 573 2 H96744 probable cytosolic
962 74 4.6 601 2 T11677 probable transcrip
963 74 4.6 604 2 S54032 probable amino aci
964 74 4.6 610 2 T22909 hypohetical prote
965 74 4.6 644 2 T20034 hypohetical prote
966 74 4.6 754 2 S48020 kinesin-related pr
967 74 4.6 855 2 A45713 Bnv transmembrane
968 74 4.6 918 2 T02759 hypohetical prote
969 74 4.6 1116 2 T31432 K-Cl cotransport p
970 74 4.6 1261 2 G81915 hypohetical prote
971 74 4.6 1217 2 F69823 probable phosphoe
972 74 4.6 1257 2 T09493 period protein hom
973 74 4.6 1445 2 T50508 hypohetical prote
974 74 4.6 1487 2 S15904 alpha-1 proteinase
975 74 4.6 1827 2 T34288 hypohetical prote
976 74 4.6 1975 2 B81192 hemagglutinin/hemo
977 74 4.6 1995 2 G81044 hemagglutinin/hemo
978 74 4.6 2013 2 A11489 probable peptidogly

979	74	4.6	3345	2	T13423	hypothetical prote	1052	73	4.5	449	2	E97428	chemotaxis motD pr
980	73.5	4.6	39	2	S24504	Ig kappa chain v r	1053	73	4.5	449	2	AF2646	chemotaxis motD pr
981	73.5	4.6	109	2	PH0089	Ig kappa chain v r	1054	73	4.5	467	1	HLMSF3	poliovirus recepto
982	73.5	4.6	110	2	PH0090	Ig light chain v r	1055	73	4.5	479	2	S18447	variant surface gl
983	73.5	4.6	198	2	T19797	hypothetical prote	1056	73	4.5	504	2	A49467	occludin - chicken
984	73.5	4.6	223	2	T19793	hypothetical prote	1057	73	4.5	538	2	T19655	hypothetical prote
985	73.5	4.6	234	2	S14237	Ig kappa chain pre	1058	73	4.5	554	2	AE0584	asparagine synthet
986	73.5	4.6	237	2	F27060	class II histocomp	1059	73	4.5	568	1	S05532	gamma-glutamyltran
987	73.5	4.6	237	2	A42013	alpha-1-B-glycopro	1060	73	4.5	568	1	T05060	hypothetical prote
988	73.5	4.6	246	1	TRRT2	trypsin (EC 3.4.21	1061	73	4.5	771	2	T50299	hypothetical serin
989	73.5	4.6	261	2	S29360	Fe gamma (IgG) rec	1062	73	4.5	793	2	AH1094	probable peptidogl
990	73.5	4.6	266	1	HLRWB	MHC class II histo	1063	73	4.5	848	2	C70203	DNA topoisomerase
991	73.5	4.6	266	2	B27618	MHC class II histo	1064	73	4.5	896	2	T47645	centromere protein
992	73.5	4.6	266	2	I54509	MHC class II HLA-D	1065	73	4.5	992	2	A39931	protein-tyrosine k
993	73.5	4.6	266	2	A39260	MHC class II histo	1066	73	4.5	1000	2	S18827	Flt3 protein - mou
994	73.5	4.6	267	2	D69404	hypothetical prote	1067	73	4.5	1048	2	T30815	platelet-derived g
995	73.5	4.6	318	2	D69742	hypothetical prote	1068	73	4.5	1090	2	C86450	F5D14.27 protein -
996	73.5	4.6	320	2	B86544	NADH (ubiquinone)	1069	73	4.5	1117	2	T19727	hypothetical prote
997	73.5	4.6	320	2	F72078	probable sodium-tr	1070	73	4.5	1167	2	A82543	chromosome segrega
998	73.5	4.6	334	2	S24440	class I histocompa	1071	73	4.5	1184	2	T09484	carilage intermed
999	73.5	4.6	356	2	F71151	probable glucosyl-1	1072	73	4.5	1191	2	T31091	hypothetical prote
1000	73.5	4.6	362	2	C35997	MHC class I histoc	1073	73	4.5	1254	2	G86379	protein F5A9.24 [i
1001	73.5	4.6	362	2	I84488	lymphocyte antigen	1074	73	4.5	1341	2	T18301	latrophilin-2, spl
1002	73.5	4.6	362	2	I54505	lymphocyte antigen	1075	73	4.5	1354	2	T18375	latrophilin-2 (spl
1003	73.5	4.6	362	2	I54314	MHC HLA-B39N - hum	1076	73	4.5	1361	2	T30884	neural specific DN
1004	73.5	4.6	362	2	I59645	MHC class I histoc	1077	73	4.5	1374	1	GNNYEC	genome polyprotein
1005	73.5	4.6	362	2	I61859	MHC class I histoc	1078	73	4.5	1407	2	T18381	latrophilin-2 (spl
1006	73.5	4.6	362	2	I61859	MHC class I histoc	1079	73	4.5	1420	2	T18385	latrophilin-2 (spl
1007	73.5	4.6	364	2	A35997	MHC class I histoc	1080	73	4.5	1820	2	A55494	latent transformin
1008	73.5	4.6	365	2	I84487	MHC HLA-A cell sur	1081	73	4.5	1856	2	C95008	immunoglobulin A1
1009	73.5	4.6	365	2	JH0544	class I histocompa	1082	73	4.5	1870	2	D88486	protein F20H11.2 [
1010	73.5	4.6	365	2	I37476	MHC class I histoc	1083	73	4.5	2143	2	G96595	hypothetical prote
1011	73.5	4.6	365	2	I37482	MHC class I histoc	1084	73	4.5	2260	2	A45259	desmoyokin - human
1012	73.5	4.6	366	2	I56034	gene HLA-C protein	1085	72.5	4.5	112	2	S38719	Ig light chain v r
1013	73.5	4.6	371	2	A8534	hypothetical 38.5K	1086	72.5	4.5	118	2	S24533	Ig kappa chain v r
1014	73.5	4.6	376	2	S70841	hypothetical trans	1087	72.5	4.5	118	2	S24507	Ig kappa chain v r
1015	73.5	4.6	394	2	T24860	hypothetical prote	1088	72.5	4.5	129	2	S40332	Ig kappa chain - h
1016	73.5	4.6	457	1	RWMST4	T-cell surface gly	1089	72.5	4.5	131	2	S40372	Ig kappa chain v-J
1017	73.5	4.6	459	2	A46254	CD4 precursor - ra	1090	72.5	4.5	131	2	B32513	Ig kappa chain pre
1018	73.5	4.6	509	2	AD0649	probable secreted	1091	72.5	4.5	237	2	H28043	MHC class II histo
1019	73.5	4.6	559	2	A45987	polypeptide N-acet	1092	72.5	4.5	247	1	TRDG	trypsin (EC 3.4.21
1020	73.5	4.6	553	2	A49722	endoglin precursor	1093	72.5	4.5	247	1	S58394	myelin/oligodendro
1021	73.5	4.6	580	2	A48143	HF-1 regulatory el	1094	72.5	4.5	252	1	HLMSBF	H-2 class II histo
1022	73.5	4.6	820	2	D71471	probable DNA mima	1095	72.5	4.5	266	1	HLH01B	MHC class II histo
1023	73.5	4.6	890	2	T00800	disease resistance	1096	72.5	4.5	266	2	I56072	MHC class II HLA-D
1024	73.5	4.6	979	2	B86207	hypothetical prote	1097	72.5	4.5	293	2	T31840	hypothetical prote
1025	73.5	4.6	1042	2	A97209	spO1D-like domain	1098	72.5	4.5	305	2	S07115	class I histocompa
1026	73.5	4.6	1066	2	T30297	dysenin heavy chain	1099	72.5	4.5	308	2	I36955	MHC class II histo
1027	73.5	4.6	1084	2	B64088	hemoglobin-binding	1100	72.5	4.5	343	1	S56493	probable alcohol d
1028	73.5	4.6	1188	2	T41696	probable C2-domain	1101	72.5	4.5	344	2	I49585	CD2 antigen protei
1029	73.5	4.6	1237	2	T08608	hypothetical prote	1102	72.5	4.5	353	2	B53250	class I histocompa
1030	73.5	4.6	1417	2	H06070	probable invasin [1103	72.5	4.5	354	2	S24433	class I histocompa
1031	73.5	4.6	1417	2	H85521	probable adhesin e	1104	72.5	4.5	354	2	I80170	class I histocompa
1032	73.5	4.6	4936	2	A83515	hypothetical prote	1105	72.5	4.5	354	2	S24438	class I histocompa
1033	73	4.5	85	2	S08109	carcinoembryonic a	1106	72.5	4.5	358	2	S03538	class I histocompa
1034	73	4.5	231	2	S45089	hypothetical prote	1107	72.5	4.5	359	1	HLHUB4	MHC class I histoc
1035	73	4.5	234	2	S26453	hypothetical prote	1108	72.5	4.5	362	2	I36962	MHC class I protei
1036	73	4.5	247	2	A55717	myelin/oligodendro	1109	72.5	4.5	362	2	I56130	HLA-B*5401 - human
1037	73	4.5	278	1	TDRTOX	OX-2 membrane gly	1110	72.5	4.5	362	2	I84486	transmembrane gly
1038	73	4.5	294	2	S39606	class I histocompa	1111	72.5	4.5	362	2	I62042	MHC HLA-B cell sur
1039	73	4.5	333	1	HLW0CB	T-cell surface gly	1112	72.5	4.5	362	2	I72755	HLA-B*5602 - human
1040	73	4.5	362	2	I62045	gene HLA B-1517 pr	1113	72.5	4.5	362	2	G01230	MHC class I histoc
1041	73	4.5	365	2	I38439	MHC class I histoc	1114	72.5	4.5	362	2	I59633	MHC HLA-B transmem
1042	73	4.5	365	2	I56039	HLA-A30.3 precurs	1115	72.5	4.5	362	2	I72753	HLA-B*5502 - human
1043	73	4.5	365	2	I61856	MHC class I histoc	1116	72.5	4.5	362	2	I59654	major histocompati
1044	73	4.5	365	2	I38518	HLA-A-0102 allele	1117	72.5	4.5	362	2	I72754	HLA-B*5601 - human
1045	73	4.5	366	2	I54430	MHC class I histoc	1118	72.5	4.5	362	2	I61863	MHC HLA-B*46 - hum
1046	73	4.5	383	2	S29733	cysteine synthase	1119	72.5	4.5	362	2	S77956	MHC class I histoc
1047	73	4.5	390	2	T09000	probable dehydroge	1120	72.5	4.5	362	2	I72752	HLA-B*5501 - human
1048	73	4.5	401	2	C95986	site-specific DNA-	1121	72.5	4.5	362	2	I61903	MHC class I histoc
1049	73	4.5	415	2	S00543	T-cell surface gly	1122	72.5	4.5	362	2	I62043	MHC HLA-B cell sur
1050	73	4.5	432	2	S30193	transcription fact	1123	72.5	4.5	362	2	I37520	MHC class I histoc
1051	73	4.5	433	2	S26646		1124	72.5	4.5	362	2	I62041	MHC HLA-B cell sur

1125	72.5	4.5	362	2	I62044	MHC class I histoc	1198	72	4.5	756	2	C84682	hypothetical prote
1126	72.5	4.5	362	2	I61860	MHC HLA-B18 chain	1199	72	4.5	873	2	JC7079	homeobox protein Z
1127	72.5	4.5	362	2	S16789	class I histocompa	1200	72	4.5	901	2	JE0062	core protein VP3 -
1128	72.5	4.5	362	2	S25415	class I histocompa	1201	72	4.5	1188	2	T46608	zinc finger protei
1129	72.5	4.5	365	2	A45847	MHC class I histoc	1202	72	4.5	1389	2	T03273	embryogenesis tran
1130	72.5	4.5	366	2	I61866	MHC HLA-Cw2.2 chai	1203	72	4.5	1404	2	T19277	hypothetical prote
1131	72.5	4.5	369	2	T48720	translaton initia	1204	72	4.5	1582	2	AC1153	adhesin homolog lm
1132	72.5	4.5	396	1	JH0631	cellular tumor ant	1205	72	4.5	1647	2	T49412	hypothetical prote
1133	72.5	4.5	432	1	RWC274	T-cell surface gly	1206	72	4.5	2256	2	AD1018	large repetitive p
1134	72.5	4.5	452	2	AG1339	hypothetical prote	1207	72	4.5	2364	2	T40884	cytotoxin L - Clo
1135	72.5	4.5	510	2	C84718	probable kinesin 1	1208	72	4.5	4351	2	T00252	MEGF1 protein - ra
1136	72.5	4.5	608	2	T03476	conserved hypothet	1209	71.5	4.5	99	2	S24501	ig kappa chain V r
1137	72.5	4.5	649	2	D85135	hypothetical prote	1210	71.5	4.5	102	2	S14590	ig kappa chain V r
1138	72.5	4.5	682	2	H87409	3-phytase, fusion,	1211	71.5	4.5	103	2	PH1043	ig light chain V r
1139	72.5	4.5	686	2	T25987	hypothetical prote	1212	71.5	4.5	103	2	PH1043	ig light chain V r
1140	72.5	4.5	727	2	S24532	hypothetical prote	1213	71.5	4.5	110	2	S26335	ig kappa chain V r
1141	72.5	4.5	743	2	T15062	hypothetical prote	1214	71.5	4.5	114	2	A32967	ig kappa chain V-I
1142	72.5	4.5	752	2	G90599	hypothetical prote	1215	71.5	4.5	118	2	S24536	ig kappa chain V r
1143	72.5	4.5	809	1	S43217	ubiquitin-protein	1216	71.5	4.5	118	2	S24503	ig kappa chain V r
1144	72.5	4.5	827	2	T20492	hypothetical prote	1217	71.5	4.5	118	2	S24535	ig kappa chain V r
1145	72.5	4.5	856	2	G70483	pyruvate water di	1218	71.5	4.5	118	2	S24500	ig kappa chain V r
1146	72.5	4.5	859	2	S24571	env protein - huma	1219	71.5	4.5	118	2	S24532	ig kappa chain V r
1147	72.5	4.5	868	1	VCLJH4	env polyprotein -	1220	71.5	4.5	119	2	A49032	ig kappa chain V r
1148	72.5	4.5	1034	2	S36758	mgli protein - mou	1221	71.5	4.5	155	2	A41675	telokin - rabbit
1149	72.5	4.5	1052	2	H83909	cell wall-associat	1222	71.5	4.5	157	2	S62571	probable ubiquitin
1150	72.5	4.5	1084	2	T18292	nicotinamide nucle	1223	71.5	4.5	210	2	JC4788	sodium channel pro
1151	72.5	4.5	1092	2	JX0312	differentiation-st	1224	71.5	4.5	220	2	A25925	class II histocomp
1152	72.5	4.5	1299	2	A86366	T26J12.6 protein -	1225	71.5	4.5	247	2	JT0555	MHC class II histo
1153	72.5	4.5	1300	2	A36502	insulin receptor-r	1226	71.5	4.5	259	2	C85630	hypothetical prote
1154	72.5	4.5	1287	2	T21312	hypothetical prote	1227	71.5	4.5	259	2	JC7109	Str2v protein - hum
1155	72.5	4.5	2356	2	T27790	hypothetical prote	1228	71.5	4.5	263	1	HLRTBB	class II histocomp
1156	72.5	4.5	3051	2	S42373	hypothetical prote	1229	71.5	4.5	266	1	HLHU3D	MHC class II histo
1157	72.5	4.5	3418	1	G02334	breast cancer tumo	1230	71.5	4.5	266	2	I54287	gene HLA-DRB1 prot
1158	72.5	4.5	3562	2	A47171	chondroitin sulfat	1231	71.5	4.5	266	2	I54287	class II histocomp
1159	72	4.5	114	2	P70181	ig heavy chain V r	1232	71.5	4.5	279	2	S04693	T-cell receptor de
1160	72	4.5	115	1	K2HUCM	ig kappa chain V-I	1233	71.5	4.5	327	2	S39604	class I histocompa
1161	72	4.5	226	2	JC5327	adhesin complex 25	1234	71.5	4.5	335	2	A53434	cell surface glyco
1162	72	4.5	231	1	TRPGTR	trypsin (RC 3.4.21	1235	71.5	4.5	337	2	S31131	hypothetical prote
1163	72	4.5	235	2	S25058	ig kappa chain - m	1236	71.5	4.5	340	2	F88545	protein P59B2.11 (
1164	72	4.5	254	2	B73266	conserved hypothet	1237	71.5	4.5	347	2	H75427	S-layer-like array
1165	72	4.5	263	2	A25911	H-2 class II histo	1238	71.5	4.5	350	2	I50015	MHC class I protei
1166	72	4.5	290	2	F42527	B16R protein - vac	1239	71.5	4.5	354	2	S24436	class I histocompa
1167	72	4.5	296	2	T23380	hypothetical prote	1240	71.5	4.5	354	2	S24437	class I histocompa
1168	72	4.5	315	1	HNZVVT	hemagglutinin prec	1241	71.5	4.5	357	2	S11139	class I histocompa
1169	72	4.5	321	2	A42507	F5L protein - vacc	1242	71.5	4.5	361	2	I54418	MHC class I histoc
1170	72	4.5	322	2	E36213	hypothetical prote	1243	71.5	4.5	362	2	I37120	MHC class I histoc
1171	72	4.5	351	2	G92755	conserved hypothet	1244	71.5	4.5	362	2	B30345	MHC class I histoc
1172	72	4.5	355	2	I80171	class I histocompa	1245	71.5	4.5	362	2	A45834	MHC class I histoc
1173	72	4.5	357	2	S12169	isopenicillin N ac	1246	71.5	4.5	362	2	I61907	MHC class I histoc
1174	72	4.5	360	2	A27638	MHC class I histoc	1247	71.5	4.5	362	2	I81233	lymphocyte antigen
1175	72	4.5	363	2	JH0542	class I histocompa	1248	71.5	4.5	362	2	I37522	MHC class I histoc
1176	72	4.5	363	2	JH0542	class I histocompa	1249	71.5	4.5	362	2	I61904	MHC class I histoc
1177	72	4.5	363	2	S03537	class I histocompa	1250	71.5	4.5	362	2	I54457	MHC class I lympho
1178	72	4.5	366	1	HLHUW3	MHC class I histoc	1251	71.5	4.5	362	2	I56133	MHC class I protei
1179	72	4.5	366	2	J50262	class I histocompa	1252	71.5	4.5	362	2	I84490	lymphocyte antigen
1180	72	4.5	370	2	AC1272	alanine dehydrogen	1253	71.5	4.5	362	2	I54298	gene HLA-B protein
1181	72	4.5	406	2	AH1822	geranyleranyl hyd	1254	71.5	4.5	362	2	A30345	MHC class I histoc
1182	72	4.5	406	2	A10621	probable bacterioph	1255	71.5	4.5	362	2	A45880	MHC class I histoc
1183	72	4.5	434	2	T47748	alpha-galactosidas	1256	71.5	4.5	362	2	S24435	class I histocompa
1184	72	4.5	469	2	S61632	glycine hydroxymet	1257	71.5	4.5	362	2	S24434	class I histocompa
1185	72	4.5	541	2	T40745	probable histidine	1258	71.5	4.5	366	2	I38505	MHC class I histoc
1186	72	4.5	548	2	T25401	hypothetical prote	1259	71.5	4.5	393	2	JC6179	dorsal switch prot
1187	72	4.5	553	1	I46329	cell fusion glycop	1260	71.5	4.5	417	2	T01616	hypothetical prote
1188	72	4.5	553	1	VGNZND	cell fusion glycop	1261	71.5	4.5	442	2	D36718	dhynrolipoamide S
1189	72	4.5	565	2	I41061	flagellin - Escher	1262	71.5	4.5	470	2	S22080	ig heavy chain pre
1190	72	4.5	583	2	S29961	Ref(2)Pp protein -	1263	71.5	4.5	491	2	F81655	conserved hypothet
1191	72	4.5	590	2	S29964	ref(2)Pn protein -	1264	71.5	4.5	530	2	D70476	DNA helicase - Aqu
1192	72	4.5	594	2	C71661	penicillin-binding	1265	71.5	4.5	536	2	S71332	natriuretic peptid
1193	72	4.5	595	2	B48658	flagellin - Escher	1266	71.5	4.5	547	1	A32244	60K cysteine-rich
1194	72	4.5	633	2	T19189	hypothetical prote	1267	71.5	4.5	566	2	G81151	single-stranded-DN
1195	72	4.5	643	2	T04847	probable serine/th	1268	71.5	4.5	583	2	T04327	phosphoglucmutase
1196	72	4.5	676	2	T47526	protein kinase-lik	1269	71.5	4.5	583	2	T04326	phosphoglucmutase
1197	72	4.5	711	2	C84767	hypothetical prote	1270	71.5	4.5	599	2	S06785	gene ref(2)P prote

1271	71.5	4.5	610	2	A11110	two-component sens	1344	71	4.4	879	2	A47704	endoglucanase I (E
1272	71.5	4.5	621	2	A71961	90Kda chaperone -	1345	71	4.4	881	2	AE2153	DNA topoisomerase
1273	71.5	4.5	648	2	A85600	hypothetical prote	1346	71	4.4	961	2	T32493	unc-45 protein - C
1274	71.5	4.5	648	2	E90749	hypothetical prote	1347	71	4.4	1106	1	PFHUGB	placeter-derived g
1275	71.5	4.5	664	2	S59638	glucose transport	1348	71	4.4	1443	2	T31896	hypothetical prote
1276	71.5	4.5	664	2	S59637	glucose transport	1349	71	4.4	1526	2	T19473	hypothetical prote
1277	71.5	4.5	782	2	S27833	rhostry-associated	1350	71	4.4	1882	2	T00069	hypothetical prote
1278	71.5	4.5	830	1	A44047	glycoprotein B pre	1351	71	4.4	1946	2	AE1449	hypothetical prote
1279	71.5	4.5	888	2	A71392	RNA polymerase pro	1352	71	4.4	2139	2	A35672	crumbs protein - f
1280	71.5	4.5	882	2	AC1214	fibrinogen-binding	1353	71	4.4	2409	1	A60979	veican precursor
1281	71.5	4.5	876	2	T51951	gamma-adaptin 1 [i	1354	71	4.4	4385	2	T29042	hypothetical prote
1282	71.5	4.5	898	1	A71720	hypothetical prote	1355	70.5	4.4	109	1	KVRT21	Ig kappa chain V r
1283	71.5	4.5	901	1	P3XR17	core protein vp3 -	1356	70.5	4.4	112	2	S38716	Ig light chain V r
1284	71.5	4.5	901	2	S07419	core protein p3 -	1357	70.5	4.4	112	2	A31807	Ig kappa chain V r
1285	71.5	4.5	1008	2	T33672	hypothetical prote	1358	70.5	4.4	113	2	PL0205	anti-DNA autoantib
1286	71.5	4.5	1059	2	T22545	hypothetical prote	1359	70.5	4.4	113	2	B41940	Ig light chain V r
1287	71.5	4.5	1186	2	A81928	two-component hybr	1360	70.5	4.4	121	2	H27887	Ig heavy chain V r
1288	71.5	4.5	1215	2	C61484	hypothetical prote	1361	70.5	4.4	128	1	GFHUC	glycophorin C - hu
1289	71.5	4.5	1270	2	S23464	vigilin - chicken	1362	70.5	4.4	131	2	D34904	Ig kappa chain pre
1290	71.5	4.5	1347	2	T30909	endo-1,4-beta-xyla	1363	70.5	4.4	144	2	B40098	colorectal cancer
1291	71.5	4.5	1539	2	S65775	homeotic protein H	1364	70.5	4.4	155	2	A28889	T-cell receptor al
1292	71.5	4.5	1576	2	T03277	pol protein - yeas	1365	70.5	4.4	197	2	S29593	Ig kappa chain (WM
1293	71.5	4.5	1608	2	A28182	hemolysin A - Serr	1366	70.5	4.4	218	2	S68241	monoclonal antibod
1294	71.5	4.5	1834	1	JDMU1	DNA-directed RNA p	1367	70.5	4.4	218	2	JCS810	class II histocomp
1295	71.5	4.5	1840	2	G85422	hypothetical prote	1368	70.5	4.4	237	2	C27060	MHC class II histo
1296	71.5	4.5	2529	2	B64635	toxin-like outer m	1369	70.5	4.4	237	2	B28043	MHC class II histo
1297	71.5	4.5	2535	2	A40043	notch protein homo	1370	70.5	4.4	237	2	E28043	probable transcrip
1298	71.5	4.5	2871	2	A55567	fibrillin I - bovi	1371	70.5	4.4	247	2	H83176	lymphocyte functio
1299	71	4.4	188	2	T41636	conserved hypothet	1372	70.5	4.4	250	2	A28564	MHC class II histo
1300	71	4.4	225	2	S37484	Ig kappa chain - m	1373	70.5	4.4	266	2	A39797	PD-1 protein - hum
1301	71	4.4	251	2	A12647	flagellar biosynth	1374	70.5	4.4	288	2	A55737	membrane glycoprot
1302	71	4.4	251	2	H97429	flagellar biosynth	1375	70.5	4.4	303	2	A40807	copper homeostasis
1303	71	4.4	260	2	I51342	MHC class II beta-	1376	70.5	4.4	306	2	A56344	hypothetical prote
1304	71	4.4	263	1	HLMSBK	H-2 class II histo	1377	70.5	4.4	307	2	S55596	thioredoxin reduct
1305	71	4.4	267	2	I56110	Fc-gamma RIIB-alp	1378	70.5	4.4	324	2	D64665	Ig gamma-4 chain C
1306	71	4.4	272	2	S77576	oligopeptide trans	1379	70.5	4.4	327	1	G4HU	hypothetical prote
1307	71	4.4	274	2	S33440	T-cell receptor ga	1380	70.5	4.4	328	2	E64020	teratocarcinoma gl
1308	71	4.4	311	2	JC7873	L-rhamnose-binding	1381	70.5	4.4	330	2	A29915	probable RING fing
1309	71	4.4	314	1	QXB2L	hypothetical prote	1382	70.5	4.4	333	2	A96829	natural killer cel
1310	71	4.4	350	2	B43670	sulfate-binding pr	1383	70.5	4.4	348	2	A56247	glucose-1-phosphat
1311	71	4.4	353	2	I51572	maternal protein -	1384	70.5	4.4	352	2	A75098	gene HLA B-1519 pr
1312	71	4.4	355	2	I37516	HLA-B alpha-chain	1385	70.5	4.4	362	2	I38421	RING-H2 zinc finge
1313	71	4.4	364	2	S03535	class I histocoma	1386	70.5	4.4	362	2	T51464	hypothetical prote
1314	71	4.4	365	2	S77963	MHC class I histoc	1387	70.5	4.4	380	2	B71122	cytochrome P450 10
1315	71	4.4	365	2	I54416	HLA-AW24 protein -	1388	70.5	4.4	406	2	A35401	hypothetical prote
1316	71	4.4	365	2	I54493	MHC class I histoc	1389	70.5	4.4	411	2	B70215	hypothetical prote
1317	71	4.4	366	2	I81231	lymphocyte antigen	1390	70.5	4.4	417	2	S76137	tapsin 1 homolog,
1318	71	4.4	366	2	I68712	MHC class I histoc	1391	70.5	4.4	430	2	T28143	killer cell inhibi
1319	71	4.4	409	2	A48890	transcription acti	1392	70.5	4.4	466	2	JC5897	probable papa - My
1320	71	4.4	419	2	G72328	hypothetical prote	1393	70.5	4.4	515	1	VGBBHB	glycoprotein gill
1321	71	4.4	439	1	AJECOG	phosphoribosylamin	1394	70.5	4.4	521	1	VGBBHB	GDSL protein - yea
1322	71	4.4	438	1	HVRKCS	Ig mu chain C regi	1395	70.5	4.4	522	2	S60483	cell fusion glycop
1323	71	4.4	445	2	H71171	probable NADH oxid	1396	70.5	4.4	538	1	B60004	DNA repair protei
1324	71	4.4	459	2	T04808	hypothetical prote	1397	70.5	4.4	559	2	A10135	ABC transporter, m
1325	71	4.4	461	1	HVRKCO	Ig mu chain C regi	1398	70.5	4.4	564	2	AG2823	afub (AE006182) [i
1326	71	4.4	508	2	S54264	glycoprotein 9C -	1399	70.5	4.4	564	2	P97601	phosphoglucumutase
1327	71	4.4	514	2	S72443	DNA-binding protei	1400	70.5	4.4	583	2	T12574	K12h4.7 protein -
1328	71	4.4	538	2	S52472	cell fusion protei	1401	70.5	4.4	585	2	S44851	envlysin [SC 3.4.
1329	71	4.4	540	1	OYHUCR	natruietic peptid	1402	70.5	4.4	587	2	S41409	hypothetical prote
1330	71	4.4	551	2	G72865	chitinase - Autogr	1403	70.5	4.4	593	2	H84779	fibulin 1 precuso
1331	71	4.4	567	2	S69779	adhesin AP65-2 pre	1404	70.5	4.4	601	2	B36346	hypothetical prote
1332	71	4.4	591	2	F64334	acetylactate synth	1405	70.5	4.4	603	2	T46236	chaperone and heat
1333	71	4.4	595	2	A48658	flagellin - Escher	1406	70.5	4.4	621	2	B45986	apical membrane an
1334	71	4.4	621	2	B57431	myosin-binding C-p	1407	70.5	4.4	622	2	B45986	probable ABC trans
1335	71	4.4	639	2	G88839	protein C10C6.5 [i	1408	70.5	4.4	648	1	G64826	fibulin 1 precuso
1336	71	4.4	690	2	S41009	hypothetical prote	1409	70.5	4.4	683	2	C36346	probable TonB-depe
1337	71	4.4	705	2	E88564	protein T0SG5.9 [i	1410	70.5	4.4	694	2	A83126	desmocollin 1b pre
1338	71	4.4	710	2	E83360	conserved hypothet	1411	70.5	4.4	770	2	B48910	probable McrB peni
1339	71	4.4	772	1	G89760	probable 5'-nucleo	1412	70.5	4.4	781	2	H95392	desmocollin 1a pre
1340	71	4.4	809	1	IJBODD	desmocollin 2a pre	1413	70.5	4.4	824	2	A48910	Deca precursor -
1341	71	4.4	863	1	IJBODC	hypothetical prote	1414	70.5	4.4	840	2	I37281	Decib precursor -
1342	71	4.4	867	2	T21311	S-layer protein pr	1415	70.5	4.4	894	2	I37282	receptor tyrosine
1343	71	4.4	874	2	JC4930		1416	70.5	4.4	983	2	A45583	

1417 70.5 4.4 1012 2 B97326 endoglucanase fami
1418 70.5 4.4 1095 2 PC1114 SKDC25 protein -
1419 70.5 4.4 1237 2 A54080 protein-tyrosine-p
1420 70.5 4.4 1279 2 T13613 hypothetical prote
1421 70.5 4.4 1331 2 T04938 hypothetical prote
1422 70.5 4.4 1331 2 AB1843 hypothetical prote
1423 70.5 4.4 1475 2 S42718 nuclear pore compl
1424 70.5 4.4 1483 2 C97012 probably celluloso
1425 70.5 4.4 1495 2 A85240 hypothetical prote
1426 70.5 4.4 1495 2 T10649 hypothetical prote
1427 70.5 4.4 1817 2 AD2185 two-component hybr
1428 70.5 4.4 2015 2 B81989 hypothetical prote
1429 70.5 4.4 2149 2 C96695 ribulose biphosph
1430 70.5 4.4 2441 2 S39161 CREB-binding prote
1431 70.5 4.4 2459 2 AF2136 peptide synthetase
1432 70.5 4.4 2468 2 A83412 hypothetical prote
1433 70.5 4.4 2479 2 F87386 conserved hypothet
1434 70.5 4.4 2616 2 A57096 model protein prec
1435 70 4.4 127 2 S04574 Ig kappa chain pre
1436 70 4.4 162 2 T51668 tumor suppressor -
1437 70 4.4 188 2 AF1062 phage polarity sup
1438 70 4.4 194 2 H97045 hypothetical prote
1439 70 4.4 215 2 JE0244 Ig kappa chain NIG
1440 70 4.4 232 1 HLM522 H-2 class II hsto
1441 70 4.4 257 2 A71081 hypothetical prote
1442 70 4.4 261 2 T52518 sperm acrosome ant
1443 70 4.4 267 2 A35902 Fc gamma (IgG) rec
1444 70 4.4 268 2 C71872 hypothetical prote
1445 70 4.4 269 2 T51539 MHC class II beta-
1446 70 4.4 324 1 ZFECS signal peptidase I
1447 70 4.4 324 2 B81058 signal peptidase I
1448 70 4.4 324 2 H85902 signal peptidase I
1449 70 4.4 334 2 AH0300 conserved hypothet
1450 70 4.4 340 2 B69446 hypothetical prote
1451 70 4.4 347 2 S09274 Ig alpha chain C r
1452 70 4.4 358 2 AE2836 lytic murein trans
1453 70 4.4 358 2 H97613 hypothetical prote
1454 70 4.4 361 2 T34361 hypothetical prote
1455 70 4.4 382 2 T39780 subtilisin (EC 3.4
1456 70 4.4 390 2 E81408 probable periplasm
1457 70 4.4 410 2 AB0735 conserved hypothet
1458 70 4.4 411 2 S07472 alpha-galactosidas
1459 70 4.4 441 2 S62538 hypothetical coile
1460 70 4.4 442 2 D95124 glycosyl transfera
1461 70 4.4 473 2 B21159 cell surface antig
1462 70 4.4 479 1 VGBEF2 glycoprotein F - h
1463 70 4.4 499 2 E84776 hypothetical prote
1464 70 4.4 544 2 A47726 dis1-suppressing p
1465 70 4.4 565 2 S29348 glycine hydroxymet
1466 70 4.4 569 2 T22516 hypothetical prote
1467 70 4.4 592 2 D88712 protein C17H12.4 [
1468 70 4.4 599 2 S29963 Ref (2)Poz protein
1469 70 4.4 656 2 E71080 probable DNA-bindi
1470 70 4.4 690 2 B82409 alpha-amylose VCA0
1471 70 4.4 855 2 T10665 hypothetical prote
1472 70 4.4 895 2 T54343 dystroglycan - hum
1473 70 4.4 925 2 S50430 hypothetical prote
1474 70 4.4 1014 2 T31109 myosin III - Atlan
1475 70 4.4 1098 1 PFMSRB platelet-derived g
1476 70 4.4 1107 2 B91271 probable periplasm
1477 70 4.4 1107 2 B96112 probable periplasm
1478 70 4.4 1107 2 E85226 hypothetical 123.8
1479 70 4.4 1178 2 S30431 MSP-300 protein -
1480 70 4.4 1193 2 S68218 botulinum neurotox
1481 70 4.4 1212 2 T44236 hypothetical prote
1482 70 4.4 1226 2 S44824 F54F2.1 protein -
1483 70 4.4 1232 2 T05322 hypothetical prote
1484 70 4.4 1448 2 A12007 Subtilase family p
1485 70 4.4 1690 2 T40847 probable rRNA biog
1486 70 4.4 1875 2 A36429 integrin beta-4 ch
1487 70 4.4 1919 2 T40032 hypothetical prote
1488 70 4.4 2182 1 GNNYB1 genome polyprotein
1489 70 4.4 2201 1 GNNYA9 genome polyprotein

1490 70 4.4 2228 2 E97942 beta-galactosidase
1491 70 4.4 2477 1 SJCHA spectrin alpha cha
1492 70 4.4 2664 2 T28626 variant-specific s
1493 70 4.4 3124 2 A40020 collagen alpha 1(X
1494 70 4.4 4135 2 T42829 tenascin-X - bovin
1495 69.5 4.3 92 2 S37502 Ig kappa chain V r
1496 69.5 4.3 102 2 S14591 Ig kappa chain V r
1497 69.5 4.3 102 2 S14594 Ig kappa chain V r
1498 69.5 4.3 107 2 S12954 Ig kappa chain V r
1499 69.5 4.3 111 2 S40359 Ig kappa chain V-J
1500 69.5 4.3 111 2 FL0257 Ig kappa chain V r

ALIGNMENTS

RESULT 1

S56749
functional adhesion molecule precursor - human
N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: A59406; S56749
R;Osaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K
J. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi
A;Reference number: A59406; MUID:99323940; PMID:10395639
A;Accession: A59406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <OZA>
A;Cross-references: UNIPROT:Q9Y624; UNIPARC:UPI0000000DC1; GB:AAD42050; NID:G5326797; P1
R;Naik, U.P.; Ehrlich, V.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a
A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Accession: S56749
A;Molecule type: protein
A;Residues: 28-49 'X', 51-53:62-73 'E', 75-103:123 'F', 125-130:'FDKDXTYILNXY','LT', 206.'X'
A;Cross-references: UNIPARC:UPI00001468C7; UNIPARC:UPI00001468CD; UNIPARC:UPI00001468D1;
C;Note: the order of the peptides other than the amino terminus was not determined
C;Genetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 25.2%; Score 404; DB 2; Length 299;
Best Local Similarity 35.2%; Pred. No. 1.9e-24;
Matches 102; Conservative 46; Mismatches 126; Indels 16; Gaps 7;

Qy 2 ARSRHRLLLLLRYLV--VALGVHKAYGFSAPKQOVTVAVEQBAILELACKTPKTVSS 59
Db 5 AQVERKLLCLFILLAILLCSLALG-----SVTVHSSEPEVRIPENNPKVLSGAYSGFS-SP 58
Qy 60 RLEWK-KLGRSVSPVYQOOLTQGDPKRAEMIDFNIRIKNVTSDACKYRCEVSAPSEOG 118
Db 59 RVEWKFPQOQUTRLVCYNNKITASYEDRVTFPLGTFTKSVTRDTCTYTCWVS--BEGG 116
Qy 119 QNLIEDTPTTLEVLVAPVSPCEVPSSALSGTVVELRCQDKGNPAPRYTFWKQIRLLEN 178
Db 117 NSYGEVKVKLVLPVPPSPKPTVNPSSATIGNRAVLTCSEQDGGSPSPSYTFWKDGVMPN 176
Qy 179 PRIGSQSTNSYTNWTKTGLQFNTVSKLTGTGYSCEARNISGVGRCPGK-RMQVDLNI 237
Db 177 PKSTRAFNSNSYLVNPTTGLBFLDPLASDTGYSCEARNISGVGRCPGK-RMQVDLNI 236
Qy 238 SGIIAAVVVALVSVCGLVGVCVAQRKGYFSKETSFOKSNSSSKATTMSE 287
Db 237 GVIVAAVLVTLILGILVFGIWFAYSRGHFDK-----TKGTSSKKVIYSQ 282

RESULT 2

JC7780

coxackie- and adenovirus receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C:Accession: JC7780
R:Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A:Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor
A:Reference number: JC7780
A:Contents: Liver
A:Accession: JC7780
A:Molecule type: mRNA
A:Residues: 1-365 <THO>
A:Cross-references: UNIPROT:Q8MWJ3; UNIPARC:UPI00000889CD; GB:AY033651
C:Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match 12.9%; Score 206.5; DB 2; Length 365;
Best Local Similarity 24.3%; Pred. No. 9.3e-09;
Matches 80; Conservative 49; Mismatches 135; Indels 65; Gaps 11;

QY 12 LLRLYLVALGYHKAYGFSAPKQDVVAVYQEAIALACK---TPKKTSSRLSEW----- 63

Db 3 LLRLFLLCGVADFTGLSTTPEQMIERAKGETAYLPCKFTGLGPDQGLDIEWLLSPA 62

QY 64 --KKL-----GRSVSFVYVYQQTLOGDFKRAEMI-----DFNIRIKNVTNRSDAGK 106

Db 63 DNOKVQVILYSGDKIYDDYQ-----DLKGRVHFTSNDLKSGLDASINVTNLQLSDIGT 117

QY 107 YRCEV-SAPSEQONLEEDVTLEVLVAPVPSCEVPSSALSCTVVVELRCODEKGNPAPE 165

Db 118 YQCKVKAPGVGNKKIQ-----ITVLKPSGIRCYVDGSEEGNDPFLKCEPKGSLPLR 172

QY 166 YTWFKDGIRLLENPRLGSSQSTNSYTMNTKTGLTFQNTVSKLDTGBYSCEARNVGYRRC 225

Db 173 YEWQK-----LSDSQKLPSTWLPMTSPVISVKNASAEYSYVYCTVTRNRVSGDQC 223

QY 226 -----PKRMQVDDLNISGIIAAVVVVVALVISVGLGVCVAQRKGVSFETSQ--- 274

Db 224 LLRLDVVPPSNRAGTAGIVGTLALVLIALVIFCC-----KKRBEKEVEKEVHHDIR 279

QY 275 -----KSNSSKATTSNENQVWLTVP 298

Db 280 DVPPPKSRISTARSYIGSNHSLGSMSPS 308

RESULT 3

A41054
fasciclin II, transmembrane splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004
C:Accession: A41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: A41054
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-811 <GRE>
A:Cross-references: UNIPROT:P34082; UNIPARC:UPI000002A963; GB:M77165; NID:G157402; PID:G157402
C:Genetics:
A:Gene: FlyBase:Fa2
A:Cross-references: FlyBase:FBgn0000635
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like type III domain
C:Keywords: membrane protein

Query Match 11.5%; Score 184; DB 2; Length 811;
Best Local Similarity 27.2%; Pred. No. 1.5e-06;
Matches 53; Conservative 37; Mismatches 75; Indels 30; Gaps 8;

QY 30 SAPKQQVAVYQEAIALACKTPKKTSSRLSEWKKLG---RSVSFVYVYQQTLOGDFKNR 86

Db 142 NAPENQYPTLGQDY---VVMCEV-KADPNPTIDWLRNGDPPIRTNDKYVYVQT----- 189

QY 87 AEMIDFNIRIKNVTNRSDAGKYRCEVSAPSEQONLEEDVTLEVLVAPVPSCEVPSSAL 146

Db 190 -----NGLLIRNVQESDEGIYTCR-AAVIETGELLER-TIRVEVFIQPBIIISLPTNLEAV 242

QY 147 SCTVVVELRCODEKGNPAPEYTWFKDGIRLLENPRLGSSQSTNSYTMNTKTGLTFQNTVSK 206

Db 243 EKPFAANCTAR-GKPVPEISWIRDATQL-----NVATADRFPQVNPQTGLVTISSVSQ 294

QY 207 LDTGBYSCEARNVSVG 221

Db 295 DDYGYTYTCLAKNRAG 309

RESULT 4

B41054

fasciclin II PI-linked splice form precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
C:Accession: B41054
R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
Cell 67, 45-57, 1991
A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
A:Reference number: A41054; MUID:92005695; PMID:1913818
A:Accession: B41054
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-873 <GRE>
A:Cross-references: UNIPARC:UPI0000177B17; GB:M77166
A:Gene: FlyBase:Fa2
A:Cross-references: FlyBase:FBgn0000635
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like type III domain
C:Keywords: transmembrane protein

Query Match 11.5%; Score 184; DB 2; Length 873;

Best Local Similarity 27.2%; Pred. No. 1.6e-06;
Matches 53; Conservative 37; Mismatches 75; Indels 30; Gaps 8;

QY 30 SAPKQQVAVYQEAIALACKTPKKTSSRLSEWKKLG---RSVSFVYVYQQTLOGDFKNR 86

Db 142 NAPENQYPTLGQDY---VVMCEV-KADPNPTIDWLRNGDPPIRTNDKYVYVQT----- 189

QY 87 AEMIDFNIRIKNVTNRSDAGKYRCEVSAPSEQONLEEDVTLEVLVAPVPSCEVPSSAL 146

Db 190 -----NGLLIRNVQESDEGIYTCR-AAVIETGELLER-TIRVEVFIQPBIIISLPTNLEAV 242

QY 147 SCTVVVELRCODEKGNPAPEYTWFKDGIRLLENPRLGSSQSTNSYTMNTKTGLTFQNTVSK 206

Db 243 EKPFAANCTAR-GKPVPEISWIRDATQL-----NVATADRFPQVNPQTGLVTISSVSQ 294

QY 207 LDTGBYSCEARNVSVG 221

Db 295 DDYGYTYTCLAKNRAG 309

RESULT 5

T29757

protein UNC-89 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C:Accession: T29757
R:Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid C09D1.
A:Reference number: Z20679
A:Accession: T29757
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-6642 <DUZ>
A:Cross-references: UNIPARC:UPI0000017CF3C; EMBL:AF003131; FIDN:AAB54132.1; GSPDB:GN00019.1
A:Experimental source: strain Bristol N2; clone C09D1
C:Genetics:

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane
F;830-1165/Domain: protein kinase homology <kin>
F;838-846/Region: protein kinase ATP-binding motif

Query Match 10.1%; Score 162; DB 2; Length 1367;
Best Local Similarity 24.7%; Pred. No. 0.00015;
Matches 55; Conservative 23; Mismatches 81; Indels 64; Gaps 7;

QY 35 QQVTVAVEQEAILACKTPKTKTSSRLLEWKLGRSVFVYQQTLOGDFKRAEMIDFN- 93
Db 554 QPAAQPTQEBSVLLCTADRNTEFN-LTWYKLGASQATSVHMGSLTPVCNKLDALWKLNG 612
QY 94 -----IRIKNVTSDAGKYRC-----EVSAPSEOGQNL 121
Db 613 TPFNSNTNDLIIVAFQNASQDQGVVCSAQDKTKKRGCLVQLIILERNMAMITG-NL 671
QY 122 EBDTVTLLEVLVAPVPSCVPSFSSALSGTGVVELRCQKQEGNPAPETWFKDGIRLLENPLR 181
Db 672 ENQTTI-----GETIEVTC-PASGNPTPHITWFKDNETLVEDSGI 711
QY 182 GSOSTSSSYMTWTKTGLQNTVSKLDTGBYSCEARNSVGYRR 224
Db 712 VLRDGNNRLTI-----RRVRKEDGGLYTCQACNVLGAR 745

RESULT 9

A27681
non-specific cross-reacting antigen precursor - human
N;Alternate names: NCA; TEX/NCA
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C;Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R;Oikawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A;Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene
A;Reference number: A26902; MUID:87298464; PMID:3619891
A;Accession: A26902
A;Molecule type: DNA
A;Residues: 1-141 <OK>
A;Cross-references: UNIPARC:UPI0000177070; GB:M16337
R;Thompson, J.A.; Paxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, C
Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
A;Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami
A;Reference number: A29875; MUID:87204248; PMID:3033672
A;Accession: A29875
A;Molecule type: DNA
A;Residues: 23-141 <THO>
A;Cross-references: UNIPARC:UPI0000177070; GB:M16337
A;Note: the authors translated the codon ACT for residue 64 as Tyr
R;Tawaragi, Y.; Oikawa, S.; Matsuoka, Y.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 150, 89-96, 1988
A;Title: Primary structure of non-specific crossreacting antigen (NCA), a member of carc
A;Reference number: A27681; MUID:88106638; PMID:3337731
A;Accession: A27681
A;Molecule type: mRNA
A;Residues: 1-238, 'V', 240-344 <TAW>
A;Cross-references: UNIPARC:UPI000012748C; GB:M18728; NID:g189084; PIDN:AA59907.1; PID:
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family; characterization of cDNAs coding for NCA and C
A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: B31037
A;Molecule type: mRNA
A;Residues: 1-137, 'L', 139-344 <BAR>
A;Cross-references: UNIPARC:UPI000016ADC6; GB:M29541; NID:g189103; PIDN:AA59915.1; PID:
A;Note: the authors translated the codon TTG for residue 138 as Phe
R;Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A;Title: Characterization of a cDNA clone for the non-specific cross-reacting antigen (NC
A;Reference number: A29918; MUID:88139389; PMID:2830274
A;Accession: A29918
A;Molecule type: mRNA
A;Residues: 1-344 <NEU>

A;Cross-references: UNIPARC:UPI000006DFA2; GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51
R;Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A;Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind
A;Reference number: A27709; MUID:88268882; PMID:3390172
A;Accession: A27709
A;Molecule type: protein
A;Residues: 35-95/99-120;123-138,149-151, 'X', 153-162,166, 'X', 168-172, 'X', 174-193,231-235,
A;Cross-references: UNIPARC:UPI0000177071; UNIPARC:UPI0000177072; UNIPARC:UPI0000177073;
078; UNIPARC:UPI0000177079; UNIPARC:UPI000017707A
R;Hefta, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A;Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspecifi
A;Reference number: A36271; MUID:90256782; PMID:2341397
A;Accession: A36271
A;Molecule type: protein
A;Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194,204-224;233-308;310;
A;Cross-references: UNIPARC:UPI000017707B; UNIPARC:UPI000017707C; UNIPARC:UPI000017707D;
082; UNIPARC:UPI0000177083; UNIPARC:UPI0000177084
R;Faxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation s
A;Reference number: A26414; MUID:87147209; PMID:3469650
A;Accession: C26414
A;Molecule type: protein
A;Residues: 35-69 <PAX>
A;Cross-references: UNIPARC:UPI0000177085
R;Khan, W.N.; Fraetgsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembry
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Accession: E44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
A;Cross-references: UNIPARC:UPI0000177086
A;Accession: F44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-137, 'L', 139-141 <KH2>
A;Cross-references: UNIPARC:UPI0000177086
C;Comment: This protein appears to be processed at the carboxyl terminus and anchored th
C;Genetics:
A;Gene: GDB:NCA
A;Cross-references: GDB:120221; OMIM:163980
A;Map position: 19q13.2-19q13.2
A;Introns: 22/1
A;Note: the list of introns may be incomplete
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatic
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalent)
F;309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form)

Query Match 10.0%; Score 161; DB 2; Length 344;
Best Local Similarity 26.5%; Pred. No. 3.4e-05;
Matches 58; Conservative 33; Mismatches 84; Indels 44; Gaps 10;

QY 41 VRYQEAILACKTPKTKTSSRLLEWKLGRSVFVYQQTLOGDFKRAEMIDFNIRKNVT 100
Db 157 VEDKDAVFTCEPQVQNTLYLWVWV-GQSLVSPRLQLSNG-----NMTLLLSVK 206
QY 101 RSDAGKYREVPASPSQGNLEEDTTLLEVLVAPVPSCVPSA--LSTVVVELRCQDK 158
Db 207 RNDAGSYECEIQNPASANRS---DPVTLNVLVGPDGFTIS-PSKANYRPGENLNLSCH-A 261
QY 159 EGNPAPEYTFKDGIRLLENPRLGSSQSTNSSVTMTKTGLQNTVSKLDTGBYSCEARN 218

Db 262 ASNPAAQYSWFING-----TFQSTQBLFIPNITVNNSGSYMCOAHN 303
 Qy 219 SVGVRRCPG-KRMQVDLNLISG---IIAAVVVALVISV 253
 Db 304 S-----ATGLNRITVTWITVSGAPVLASAVATGITTGV 337

RESULT 10
 JN0635
 neural cell adhesion molecule 2 precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C:Accession: JN0635
 R:Tonissen, K.F.; Kriegl, P.A.
 Gene 127, 243-247, 1993

A>Title: Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus laevis are ex
 A:Reference number: JN0635; MUID:93273239; PMID:7684721
 A:Molecule type: mRNA
 A:Residues: 1-1092 <TON>
 A:Cross-references: UNIPROT:P36335; UNIPARC:UPI000012EDC7; GB:M76710; NID:G214611; PIDN:
 C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
 C:Genetics:
 A:Gene: NCAM2
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C:Keywords: alternative splicing; cell adhesion; duplication; heparin binding; sialoglyc
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-1092/Product: extracellular #status predicted <EXT>
 F:34-95/Domain: immunoglobulin homology <IMM1>
 F:129-188/Domain: immunoglobulin homology <IMM2>
 F:149-153/Region: heparin binding #status predicted
 F:158-162/Region: heparin binding #status predicted
 F:317-381/Domain: immunoglobulin homology <IMM3>
 F:413-475/Domain: fibronectin type III repeat homology <IMM4>
 F:512-589/Domain: fibronectin type III repeat homology <FN3A>
 F:619-680/Domain: fibronectin type III repeat homology <FN3B>
 F:706-723/Domain: transmembrane #status predicted <TM>
 F:724-1092/Domain: intracellular #status predicted <INT>
 F:41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
 F:219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.8%; Score 158; DB 1; Length 1092;
 Best Local Similarity 26.6%; Pred. No. 0.00024;
 Matches 55; Conservative 37; Mismatches 99; Indels 16; Gaps 8;

Qy 29 FSAPKQDV--VTAVYQEAAILACKTPKKTVSSRLWKKLGRSVSFVYQOTLQGDPKNR 86
 Db 300 YAKPKTYVENKTVLDELITLCEASGDPIPS-IWRTAHRNIS--SBEKTLDGHLVVK 356

Qy 87 AEMIDFNIRIKNTRSDAGKYRCEVSAPSQQGNLEBDTTLVLVAPVPSCEVPSSAL 146
 Db 357 DHIRMSALTLDKQYTDAGEYFCVASNPFI----GVDQMAYFEVQAPKIRG-PVVVYTW 411

Qy 147 SGTVVELRCQEGNPAPETVTFKDGIRLLENPRLSQSSTNSSTYNTTKTGLTFQNTVSK 206
 Db 412 EGNPVNITC-DVLAHPSAAVSWFRDG-QLDPS-----SNFSNIKIYNGPTFSSLEVAPDSE 465

Qy 207 LDTGEYSCEARNVGVYRRCPGKMQVD 233
 Db 466 NDFGNYNCSAVNSIGHESSEFLLVQAD 492

RESULT 11
 JCS702
 ErbB kinase activator alpha2a, brain and thymus - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 09-Jul-2004
 C:Accession: JCS702; PC4417
 R:Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag
 J. Biochem. 122, 675-680, 1997
 A>Title: A novel brain-derived member of the epidermal growth factor family that interact

A:Reference number: JCS700; MUID:98006324; PMID:9348101
 A:Accession: JCS702
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-860 <HIG>
 A:Cross-references: UNIPROT:O35569; UNIPARC:UPI000002AFB5; DDBJ:D89996; NID:G2605631; PI
 A:Experimental source: PC-12 cell
 A:Accession: PC4417
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: F', 212-213, 223-860 <HIG>
 A:Cross-references: UNIPARC:UPI000017062D; DDBJ:AB001576; NID:G2605478; PIDN:BAA23348.1;
 A:Experimental source: PC-12 cell
 C:Comment: This protein is a member of the epidermal growth factor family. It is function
 ating the differentiation of MDA-MB-453 cells.
 C:Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; immuno
 C:Keywords: glycoprotein
 F:274-327/Domain: Ig-like #status predicted <IGL>
 F:361-397/Domain: EGF homology <EGF>
 F:422-444/Domain: hydrophobic #status predicted <HYD>
 F:163,294,467/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.8%; Score 157; DB 2; Length 860;
 Best Local Similarity 27.7%; Pred. No. 0.00021;
 Matches 56; Conservative 24; Mismatches 86; Indels 36; Gaps 8;

Qy 66 LGRSVFVYQOTLQGD--FKNRAEMIDFNIRIKNTRSDAGKYRCEVSAPSQQGNLE 123
 Db 204 LKNQRIYIFLEPTEQPLVFKTAFAPVDN--GKNI-KKEVGKILCTDCATRPKLKKKKS 260

Qy 124 DTVTLVLVAPVPSCEVPSSALSGTVVELRCQEGNPAPETVTFKDGIRLLENPRLS 183
 Db 261 QTGEV-----GKQSLKCEAAGNPQPSYRMPKDGKELNR-----S 296

Qy 184 QSTNSSTYNTTKTGLTFQNTVSKLDTGEYSCEARNVGVYRRCPGKMQVDLMI-----S 238
 Db 297 RDRIKYGNGRKNRSLQFNKVKVEDAGEYVCEANILGKDTVRG-RLHNVSVSTTLSSWS 355

Qy 239 GIIAAVVVVALVISVCGLGVCY 260
 Db 356 GHARKCNETAKSYCVNG-GVCY 376

RESULT 12
 JCS701
 ErbB kinase activator alpha1, brain and thymus - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 09-Jul-2004
 C:Accession: JCS701; PC4411
 R:Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag
 J. Biochem. 122, 675-680, 1997
 A>Title: A novel brain-derived member of the epidermal growth factor family that interact
 A:Reference number: JCS700; MUID:98006324; PMID:9348101
 A:Accession: JCS701
 A:Molecule type: mRNA
 A:Residues: 1-868 <HIG>
 A:Cross-references: UNIPROT:O35569; UNIPARC:UPI0000130508; DDBJ:D89995; NID:G2605629; PI
 A:Experimental source: PC-12 cell
 A:Accession: PC4411
 A:Molecule type: protein
 A:Residues: 128-162 <HIG>
 A:Cross-references: UNIPARC:UPI0000179297
 A:Experimental source: PC-12 cell
 C:Comment: This protein is a member of the epidermal growth factor family. It is function
 ating the differentiation of MDA-MB-453 cells.
 C:Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; immuno
 F:361-397/Domain: EGF homology <EGF>

Query Match 9.8%; Score 157; DB 2; Length 868;
 Best Local Similarity 27.7%; Pred. No. 0.00021;
 Matches 56; Conservative 24; Mismatches 86; Indels 36; Gaps 8;

Qy 66 LGRSVFVYQOTLQGD--FKNRAEMIDFNIRIKNTRSDAGKYRCEVSAPSQQGNLE 123
 Db 204 LKNQRIYIFLEPTEQPLVFKTAFAPVDN--GKNI-KKEVGKILCTDCATRPKLKKKKS 260

Db	204	LEBNQRYIPLEPTEQPLVPTAFAPVDPN--GKNI-KKEVGKILCTDCATRRPLKMKKS	260
Qy	124	DTVTLEVLVAVAPVSCVPSALSGTVVLRCDKEGNPAPEYTWFKDGIIRLENPLRGS	183
Db	261	QTGEV-----GKQSLKCEAAGNPPQPSYRPFKDGKELNR-----S	296
Qy	184	QSTNSYTWMTKTGTLPNTVSKLDTGEYSCVARNVGVYRRCCKRMQVDDLNI-----S	238
Db	297	RDRIKYNGRKNSRLQFNKVKVEDAGEYVCEANILGKDTVRG-RLHVNVSVTLLSWS	355
Qy	239	GIIAAVVVVALVISVCGLGVCY	260
Db	356	CHARKCNETAKSYCVNG-GVCY	376
RESULT 13			
TDHULK			
N;Alternate names: leukocyte antigen precursor - human			
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)			
C;Species: Homo sapiens (man)			
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004			
C;Accession: S03841; JLO051			
R;Streuli, M.; Krueger, N.X.; Hall, L.R.; Schlossman, S.F.; Saito, H.			
J. Exp. Med. 168, 1523-1530, 1988			
A;Title: A new member of the immunoglobulin superfamily that has a cytoplasmic region homologous to the T cell receptor			
A;Reference number: JLO051; MID:89035978; PMID:2972792			
A;Accession: S03841			
A;Status: nucleic acid sequence not shown			
A;Molecule type: mRNA			
A;Residues: 1-1897 <STR>			
A;Cross-references: UNIPROT:P10586; UNIPARC:UPI0000132992; EMBL:Y00815; MID:g34266; PIDN:G34266			
C;Genetics:			
A;Gene: GDB:PTPRF; LAR			
A;Cross-references: GDB:120138; OMIM:179590			
A;Map position: lp34-lp34			
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogly			
F;16/Domain: signal sequence #status predicted <SIG>			
F;17-1897/Product: leukocyte antigen-related protein #status predicted <MAT>			
F;17-1250/Domain: extracellular #status predicted <EXT>			
F;17-99/Domain: immunoglobulin homology <IMM1>			
F;139-199/Domain: immunoglobulin homology <IMM2>			
F;236-290/Domain: immunoglobulin homology <IMM3>			
F;308-390/Domain: fibronectin type III repeat homology <FN3A>			
F;403-489/Domain: fibronectin type III repeat homology <FN3B>			
F;501-583/Domain: fibronectin type III repeat homology <FN3C>			
F;596-685/Domain: fibronectin type III repeat homology <FN3D>			
F;598-798/Domain: fibronectin type III repeat homology #status atypical <FN3E>			
F;810-893/Domain: fibronectin type III repeat homology <FN3F>			
F;905-989/Domain: fibronectin type III repeat homology <FN3G>			
F;1001-1078/Domain: fibronectin type III repeat homology <FN3H>			
F;1251-1274/Domain: transmembrane #status predicted <TM>			
F;1275-1897/Domain: intracellular #status predicted <INT>			
F;1285-1897/Domain: leukocyte common antigen cytosolic domain homology <LAC>			
F;1365-1586/Domain: protein-tyrosine-phosphatase homology <PTP1>			
F;1654-1877/Domain: protein-tyrosine-phosphatase homology <PTP2>			
F;144-97, 146-197, 243-288/Difaulte bonds: #status predicted			
F;107, 240, 285, 711, 956/Binding site: carbohydrate (Asn) (covalent) #status predicted			
F;1536/Active site: Cys (phosphotyrosine intermediate) #status predicted			
F;1544/Binding site: substrate phosphate (Arg) #status predicted			
F;1829/Active site: Cys (phosphotyrosine intermediate) #status predicted			
F;1835/Binding site: substrate phosphate (Arg) #status predicted			
Query Match			
Best Local Similarity 9.7%; Score 156; DB 1; Length 1897;			
Matches 59; Conservative 35; Mismatches 89; Indels 46; Gaps 10;			
Qy	11	LLRLRYLVVALGYKAYGFSAPKQQQVWTAVEYQEAAILACKT---PKKTVSSRLKWKLG	67
Db	8	LVMGLGVAGNGDSKPFVKVBDQ---TCLSGVAFVCOATGEPK----PRITWKKG	60

Qy	68	RSVSFVYVYQQTLOGDFKNRAEMIDFN-----IRIKNV-TRSDAGKYRCEVSAPSQQCN	120
Db	61	KKVS-----SQRFVIFBDDGAGSVLRIOPLRVQRDEAIYECTATNSLGEINT	108
Qy	121	LBEDTTLVLVAVAPVSC-----VPSSALSGTVVLRCDKEGNPAPEYTWFKDGIIR	174
Db	109	SAKLSVLESEQIPLPGFSPIDMGQPLKVVEKARTATML--CA-AGNPDPPEISWFKDPLP	164
Qy	175	LLENPLRGSQSTNSYTWMTKTGTLPNTVSKLDTGEYSCVARNVGVYR	223
Db	165	V-----DPATSNGRKIQLRGALQIESSESDDQKYECVATNSAGTR	206
RESULT 14			
T23007			
hypothetical protein K09C8.5 - Caenorhabditis elegans			
C;Species: Caenorhabditis elegans			
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004			
C;Accession: T23007; T23543			
R;Kershaw, J.			
submitted to the EMBL Data Library, November 1995			
A;Reference number: Z19651			
A;Accession: T23007			
A;Status: preliminary; translated from GB/EMBL/DBDJ			
A;Molecule type: DNA			
A;Residues: 1-1328 <W1>			
A;Cross-references: UNIPROT:Q21043; UNIPARC:UPI00000823FD; EMBL:Z68005; PIDN:CAA91994.1;			
A;Experimental source: clone F59F3			
R;Kershaw, J.			
submitted to the EMBL Data Library, November 1995			
A;Reference number: Z19755			
A;Accession: T23543			
A;Status: preliminary; translated from GB/EMBL/DBDJ			
A;Molecule type: DNA			
A;Residues: 1-1328 <W2>			
A;Cross-references: UNIPARC:UPI00000823FD; EMBL:Z68006; PIDN:CAA91999.1; GSPDB:GN00028;			
A;Experimental source: clone K09C8			
C;Genetics:			
A;Gene: CESP:K09C8.5			
A;Map position: X			
A;Introns: 34/1; 85/3; 133/3; 182/2; 220/3; 262/2; 390/3; 442/2; 493/3; 563/2; 586/3; 615/3			
Query Match			
Best Local Similarity 9.7%; Score 155.5; DB 2; Length 1328;			
Matches 42; Conservative 34; Mismatches 66; Indels 11; Gaps 4;			
Qy	69	SVSFVYVYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSQQCNLEEDTVTL	128
Db	382	TITWLFKQKLTERSKHKLTKNGSVLKIPIPLNTDIGOYECVASNGEESKSHI--FSVSL	439
Qy	129	EVLVAVAPVSCVPSALSGTVVLRCDKEGNPAPEYTWFKDGIIRLENPLRGSQSTNS	188
Db	440	KESEQPVIIADPMDTNATIGQQVTLRCAK--GFPVDPVVVWLPFEGIRI---PR-----RNT	490
Qy	189	SYTWMTKTGTLPNTVSKLDTGEYSCVARNVGVYR	221
Db	491	RYTISDNNIELTIEKTRHDSGVFTCAVNSVG	523
RESULT 15			
T34416			
hypothetical protein F12P3.2 - Caenorhabditis elegans			
C;Species: Caenorhabditis elegans			
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999			
C;Accession: T34416			
R;Fulton, B.; Wohldmann, P.			
submitted to the EMBL Data Library, July 1998			
A;Description: The sequence of C. elegans cosmid F12P3.			
A;Reference number: Z21521			
A;Accession: T34416			
A;Status: preliminary; translated from GB/EMBL/DBDJ			
A;Molecule type: DNA			
A;Residues: 1-2783 <FUL>			

A; Cross-references: UNIPARC:UPI000017B8E5; EMBL:U80022; PIDN:AAC25886.1; GSPDB:GNO0023;
A; Experimental source: strain Bristol N2; clone F12F3

C;Genetics:

A;Gene: CESP:F12F3.2

A:Map position: 5

A;Map position: 3
A:Introns: 45/3: 90/3: 451/3: 509/1: 2313/3: 2341/3: 2378/3: 2414/2: 2453/3: 2474/2: 252

Query Match	9.7%	Score 155.5;	DB 2;	Length 2783;
Best Local Similarity	30.4%;	Pred. No. 0.0012;		
Matches 58;	Conservative 15;	Mismatches 77;	Indels 41;	Gaps 6;
Qy	86	RAEMIDFNRIKNTVTRSDAGKYRCEVSAPSEQQGNLEEDTVTLEVLVAPAVP	-----	137
Db	2606	RNEGDKFILRIANVTRADAGKYELTAINPSQOAALELTIVQSTKTGVAKPFNEPIS	2665	
Qy	138	--SCEVPSSALSCTVTVELRCODKEGNPAEYTFWKDGIRL---	LENPLCSQSTNSSYTM	192
Db	2666	VQCEKVRARLASF-----SGTPAPACRFYNGNELIDGLDGYTITSSDNTSS---	2714	
Qy	193	NTKTGTQFNTVSKLDTGEYSCBARNVGYR-----	RCPGKMKVDDLDNLISGIIA	242
Db	2715	-----LLINSVDKKEGVELICTIRNQGHELANAMILSBGEC-RKHPRIDIVPVCNFSI	2767	
Qy	243	ANVVVALVISV	253	
Db	2768	FSVVHVLLISV	2778	

Search completed: April 26, 2006, 17:43:25
Job time : 32 secs

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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:43:09 ; Search time 226 Seconds
(without alignments)

974.004 Million cell updates/sec

Title: US-10-785-607C-9

Perfect score: 1605

Sequence: 1 MARRSRHRLLLRLVVA.....TPVPALWKAAGSGRQEF 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1475	91.9	298	1	JAM2 HUMAN
2	1172	73.0	298	1	JAM2 MOUSE
3	598.5	37.3	243	2	Q5ZJD1_CHICK
4	517.5	32.2	181	2	Q9CWD9_MOUSE
5	479	29.8	310	1	JAM3 MOUSE
6	477	29.7	310	1	JAM3 RAT
7	461.5	28.8	310	1	JAM3 HUMAN
8	445	27.7	291	2	Q66J75_XENTR
9	439.5	27.4	296	2	Q64UC0_XENLA
10	439.5	27.4	300	2	Q7SYQ7_XENLA
11	419.5	26.1	289	2	Q7ZWT0_XENLA
12	414	25.8	257	2	Q4SOM3_TETNG
13	404	25.2	299	1	JAM1 HUMAN
14	404	25.2	299	1	JAM1 MOUSE
15	402.5	25.1	298	1	JAM1 BOVIN
16	402.5	25.1	298	2	Q5E9V8_BOVIN
17	401.5	25.0	292	2	Q66I72_BRARE
18	396.5	24.7	260	2	Q4S828_TETNG
19	394	24.5	300	1	JAM1 MOUSE
20	394	24.5	300	2	Q8VC39_MOUSE
21	382	23.8	300	1	JAM1 RAT
22	379.5	23.6	273	2	Q4RRS6_TETNG
23	366.5	22.8	259	2	Q9Y5B2_HUMAN
24	284.5	17.7	173	2	Q9JKD5_RAT
25	238	14.8	319	1	Q5VZP6_MOUSE
26	238	14.8	319	2	Q5VZP6_HUMAN
27	229	14.3	335	2	Q9PMR4_CHICK
28	228	14.2	318	2	Q91664_XENLA
29	228	14.2	335	2	Q9YGH1_CHICK
30	226	14.1	319	1	Q5XGG4_MOUSE
31	225.5	14.0	347	2	Q5XGG4_XENTR

32	225.5	14.0	394	1	ESAM RAT	06ayd4 rattus norv
33	217	13.5	181	2	Q91665_XENLA	Q91665 xenopus lae
34	214	13.3	335	2	Q9YGV5_CHICK	Q9YGV5 gallus gall
35	211.5	13.2	387	2	Q86XK7_HUMAN	Q86XK7 homo sapien
36	211.5	13.2	412	2	Q6MZS4_HUMAN	Q6MZS4 homo sapien
37	210	13.1	390	1	ESAM HUMAN	Q96ap7 homo sapien
38	210	13.1	428	2	Q5U2P2_RAT	Q5U2P2 rattus norv
39	208.5	13.0	319	2	Q9TU80_CANFA	Q9TU80 canis famil
40	207.5	12.9	394	1	ESAM MOUSE	Q925f2 mus musculus
41	207	12.9	442	2	Q6NW88_BRARE	Q6NW88 brachydanio
42	206.5	12.9	365	1	QXAR_BOVIN	Q8xmv3 bos taurus
43	203.5	12.7	344	2	Q568F7_BRARE	Q568F7 brachydanio
44	201.5	12.6	332	2	Q6P359_XENTR	Q6P359 xenopus tro
45	198.5	12.4	365	1	QXAR_HUMAN	Q78310 homo sapien
46	198.5	12.4	365	1	QXAR_PONPY	Q5r764 pongo pygma
47	198	12.3	407	2	Q9D2J4_MOUSE	Q925f2 mus musculus
48	196	12.2	319	2	Q9TU79_PIG	Q9TU79 sus scrofa
49	195.5	12.2	283	2	Q4V7Q4_XENLA	Q4V7Q4 xenopus lae
50	195	12.1	404	2	Q4KDY3_RAT	Q4KDY3 rattus norv
51	194.5	12.1	431	2	Q5DX21_HUMAN	Q5dx21 homo sapien
52	194	12.1	335	2	Q588E2_XENLA	Q588E2 xenopus lae
53	194	12.1	372	1	QXAR_BRARE	Q90V50 brachydanio
54	193	12.0	390	1	ESAM_MACFA	Q95k13 macaca fasc
55	189.5	11.8	430	2	Q8N4F1_HUMAN	Q8N4F1 homo sapien
56	189.5	11.8	452	2	Q4RRTO_TETNG	Q4rrt0 tetraodon n
57	186.5	11.6	210	2	Q4R7W7_MACFA	Q4r7w7 macaca fasc
58	185	11.5	365	1	QXAR_MOUSE	Q97792 mus musculus
59	184	11.5	773	2	Q6IDE4_DROME	Q6ide4 drosophila
60	184	11.5	873	1	FAS2_DROME	F34082 drosophila
61	183	11.4	300	2	Q9DA22_MOUSE	Q9da22 mus musculus
62	183	11.4	300	2	Q9D9J0_MOUSE	Q9d9j0 mus musculus
63	182	11.3	365	1	QXAR RAT	Q9r066 rattus norv
64	182	11.3	553	2	Q5RIP6_BRARE	Q5rip6 brachydanio
65	179.5	11.2	417	2	Q5R6B7_PONPY	Q5r6b7 pongo pygma
66	179	11.2	323	2	Q8NDD2_HUMAN	Q8ndd2 homo sapien
67	179	11.2	432	2	Q6DDE7_XENLA	Q6dde7 xenopus lae
68	179	11.2	858	2	O18466_HIRME	O18466 hirudo medi
69	178	11.1	327	1	VSIG2_HUMAN	Q96ig7 homo sapien
70	178	11.1	3950	2	Q7YRP5_CANFA	Q7yrf5 canis famil
71	177.5	11.1	328	1	VSIG2_MOUSE	Q92109 mus musculus
72	177.5	11.1	395	2	Q8B2P4_MOUSE	Q8bzp4 mus musculus
73	177.5	11.1	395	2	Q8BXJ7_MOUSE	Q8bxj7 m mus muscu
74	177.5	11.1	404	2	Q8BLQ9_MOUSE	Q8blq9 mus musculus
75	177	11.0	332	2	Q640U3_XENTR	Q640u3 xenopus tro
76	177	11.0	5932	2	Q5W615_CABEL	Q5w615 caenorhabdi
77	177	11.0	6632	1	UNC89_CABEL	O01761 caenorhabdi
78	177	11.0	7122	2	Q5W616_CABEL	Q5w616 caenorhabdi
79	177	11.0	7441	2	Q5W617_CABEL	Q5w617 caenorhabdi
80	177	11.0	8081	2	Q7Z120_CABEL	Q7z120 caenorhabdi
81	176.5	11.0	848	2	Q7QCU0_ANOGA	Q7qcu0 anopheles g
82	174.5	10.9	417	2	Q7TNL1_MOUSE	Q7tnl1 mus musculus
83	174	10.8	3493	2	Q4RJ20_TETNG	Q4rj20 tetraodon n
84	173.5	10.8	404	2	Q8BYF1_MOUSE	Q8byf1 mus musculus
85	171	10.7	322	2	Q4SHQ7_TETNG	Q4shq7 tetraodon n
86	171	10.7	512	2	Q6D8N8_HUMAN	Q6d8n8 homo sapien
87	171	10.7	5635	2	Q5TVR7_HUMAN	Q5tvr7 homo sapien
88	171	10.7	5636	2	Q6R3W7_HUMAN	Q6r3w7 homo sapien
89	169.5	10.6	7962	2	Q10465_HUMAN	Q10465 homo sapien
90	169.5	10.6	34350	2	Q8WZ42_HUMAN	Q8wz42 homo sapien
91	169	10.5	428	2	Q6F3J3_MOUSE	Q6f3j3 mus musculus
92	169	10.5	443	2	Q8N2F4_HUMAN	Q8n2f4 homo sapien
93	168.5	10.5	329	2	Q8N225_HUMAN	Q8n225 homo sapien
94	168.5	10.5	1340	2	Q8NDA2_HUMAN	Q8nda2 homo sapien
95	168	10.5	344	1	CEAM6_HUMAN	P40199 homo sapien
96	168	10.5	344	2	Q53XP7_HUMAN	Q53xp7 homo sapien
97	167	10.4	582	2	Q80WN2_MOUSE	Q80wn2 mus musculus
98	167	10.4	595	2	Q68SN8_MOUSE	Q68sn8 mus musculus
99	166.5	10.4	442	2	Q9BY67_HUMAN	Q9by67 homo sapien
100	166.5	10.4	1252	2	Q96DN3_HUMAN	Q96dn3 homo sapien
101	166	10.3	795	2	Q40YMO_BRARE	Q40ym0 brachydanio
102	165.5	10.3	735	2	Q4RZE9_TETNG	Q4rze9 tetraodon n
103	165	10.3	405	2	Q6PFK4_BRARE	Q6pfk4 brachydanio
104	164.5	10.2	414	2	Q5VU13_HUMAN	Q5vul3 homo sapien

105	164.5	10.2	1038	2	Q4T3K8_TETNG	Q4t3k8 tetraodon n
106	164	10.2	837	1	NCAM2_MOUSE	O35136 mus musculus
107	163.5	10.2	373	2	Q9H6B4_HUMAN	O9h6b4 homo sapien
108	163.5	10.2	846	2	O57577_CYNPY	O57577 cynops pyrr
109	163.5	10.2	1100	2	O57576_CYNPY	O57576 cynops pyrr
110	163	10.2	433	2	O6DJ83_XENLA	O6dj83 xenopus tro
111	163	10.2	875	2	Q4RRR9_TETNG	Q4rrr9 tetraodon n
112	163	10.2	1431	2	Q80U60_MOUSE	O80u60 mus musculus
113	162.5	10.1	237	2	O6DQX5_RABIT	O6dqx5 oryctolagus
114	162.5	10.1	952	2	Q4SPY1_TETNG	Q4spy1 tetraodon n
115	162	10.1	725	2	Q73634_XENLA	O73634 xenopus lae
116	162	10.1	1345	2	Q8VCD0_MOUSE	O8vcd0 mus musculus
117	162	10.1	1367	1	VGPR2_MOUSE	O8vcd0 mus musculus
118	162	10.1	4071	2	Q6KDX1_CHICK	O6kdx1 gallus gall
119	161.5	10.1	445	2	Q8R4L1_MOUSE	O8r4l1 mus musculus
120	161.5	10.1	445	2	Q8K3T6_MOUSE	O8k3t6 mus musculus
121	161.5	10.1	979	2	Q4TBU1_TETNG	Q4tbu1 tetraodon n
122	161	10.0	344	2	Q13774_HUMAN	O13774 homo sapien
123	161	10.0	456	2	Q8R5M8_MOUSE	O8r5m8 mus musculus
124	161	10.0	727	2	Q6RKB2_RAT	O6rkb2 rattus norv
125	161	10.0	837	2	Q6RKB3_RAT	O6rkb3 rattus norv
126	160.5	10.0	1049	2	Q4RVM2_TETNG	Q4rvm2 tetraodon n
127	160.5	10.0	2693	2	Q8ISF3_CAEBL	O8isf3 caenorhabdi
128	160.5	10.0	2708	2	Q8ISF4_CAEBL	O8isf4 caenorhabdi
129	160.5	10.0	18519	2	Q8ISF6_CAEBL	O8isf6 caenorhabdi
130	160.5	10.0	18534	2	Q8ISF7_CAEBL	O8isf7 caenorhabdi
131	160	10.0	837	1	NCAM2_HUMAN	O15394 homo sapien
132	160	10.0	1209	2	Q7PG72_ANOGA	O7pg72 anopheles g
133	160	10.0	1215	2	Q7Q8C1_ANOGA	O7q8c1 anopheles g
134	159.5	9.9	226	2	Q4RDM1_TETNG	O4rdm1 tetraodon n
135	159.5	9.9	545	2	Q7Q1V4_ANOGA	O7q1v4 anopheles g
136	159.5	9.9	2528	2	Q4S2G3_TETNG	O4s2g3 tetraodon n
137	159	9.9	803	2	Q8O2F5_RAT	O8o2f5 rattus norv
138	159	9.9	837	2	Q7Z7F2_HUMAN	O7z7f2 homo sapien
139	158.5	9.9	319	2	Q7QLK4_ANOGA	O7qlk4 anopheles g
140	158.5	9.9	1048	2	Q7QH02_ANOGA	O7qh02 anopheles g
141	158	9.8	231	2	Q6S8Q7_HUMAN	O6s8q7 homo sapien
142	158	9.8	605	2	Q8TBU0_HUMAN	O8tbu0 homo sapien
143	158	9.8	673	2	Q6MZW2_HUMAN	O6mzw2 homo sapien
144	158	9.8	693	2	Q9UPU1_HUMAN	O9upu1 homo sapien
145	158	9.8	1092	1	NCAL2_XENLA	O16335 xenopus lae
146	158	9.8	1343	2	Q5POU0_RAT	O5pqou0 rattus norv
147	157.5	9.8	302	2	Q4T3Z1_TETNG	Q4t3z1 tetraodon n
148	157.5	9.8	1534	2	Q4RRJ4_TETNG	Q4rrj4 tetraodon n
149	157	9.8	435	2	Q5FWM6_XENLA	O5fwm6 xenopus lae
150	157	9.8	868	1	NRG2_RAT	O35569 rattus norv
151	157	9.8	1342	2	Q9GPF6_DROME	O9gpf6 drosophila
152	157	9.8	1342	2	Q9VPZ7_DROME	O9vpz7 drosophila
153	157	9.8	1887	2	Q9QW67_MURI	O9qw67 rattus ap.
154	156.5	9.8	435	2	Q8N3J6_HUMAN	O8nj36 homo sapien
155	156.5	9.8	437	2	Q8I2P8_HUMAN	O8ip28 homo sapien
156	156.5	9.8	779	2	Q97136_MANSE	O97136 manduca sex
157	156.5	9.8	837	2	Q97137_MANSE	O97137 manduca sex
158	156.5	9.8	893	2	Q5TNT4_ANOGA	O5tnt4 anopheles g
159	156.5	9.8	1089	2	Q4S556_TETNG	O4s556 tetraodon n
160	156.5	9.8	1378	1	ROBO2_HUMAN	O9hck4 homo sapien
161	156	9.7	276	2	Q64O85_XENTR	O64o85 xenopus tro
162	156	9.7	347	2	Q6PJ32_HUMAN	O6pj32 homo sapien
163	156	9.7	377	2	Q9VOY0_DROME	O9vgy0 drosophila
164	156	9.7	749	2	Q967D9_DROME	O967d9 drosophila
165	156	9.7	756	1	NRG2_MOUSE	O56974 mus musculus
166	156	9.7	902	2	NRG1Q17_DROME	O8iq17 drosophila
167	156	9.7	903	2	Q9VQY1_DROME	O9vgy1 drosophila
168	156	9.7	903	2	Q967D8_DROME	O967d8 drosophila
169	156	9.7	1187	2	Q589G5_CHICK	O589g5 gallus gall
170	156	9.7	1343	1	VGPR2_RAT	O8r75 rattus norv
171	156	9.7	1484	2	Q5W9G3_HUMAN	O5w9g3 homo sapien
172	156	9.7	1508	2	Q6NR34_DROME	O6nr34 drosophila
173	156	9.7	1508	2	Q9VQY2_DROME	O9vgy2 drosophila
174	156	9.7	1531	1	Q967D7_DROME	O967d7 drosophila
175	156	9.7	1897	1	PTPRP_HUMAN	P10586 homo sapien
176	156	9.7	1898	2	Q86WS0_HUMAN	O86ws0 homo sapien
177	156	9.7	1898	2	Q5T021_HUMAN	O5t021 homo sapien

O58pj6	mus musculus
Q5t022	homo sapien
O5w9g2	homo sapien
O5k373	brachydanio
O5k374	brachydanio
O4kmg2	homo sapien
Q21043	caenorhabdi
Q5h261	xenopus tro
O6ayp5	rattus norv
P31809	mus musculus
O66iv0	xenopus lae
O73633	xenopus lae
O14511	homo sapien
P61670	xenopus lae
O5ub49	homo sapien
O8nf28	homo sapien
O8nhn5	homo sapien
O8uvd6	brachydanio
O08476	gallus gall
Q48c9	tetraodon n
P98160	homo sapien
O5vu27	homo sapien
Q925p3	mus musculus
O695l3	brachydanio
Q6wzn9	rattus norv
O90241	gallus gall
O6rwt3	bos taurus
O71879	brachydanio
O91y9	gallus gall
O5t564	anopheles g
Q8mra3	drosophila
O86bd5	drosophila
Q7t6p3	mus musculus
O70623	anopheles g
Q988w4	brachydanio
Q502i0	brachydanio
Q4t426	tetraodon n
Q7pv30	anopheles g
O8bj45	mus musculus
Q925p2	mus musculus
O8n475	homo sapien
Q4rvz3	tetraodon n
Q90ym2	brachydanio
O98918	gallus gall
O6van5	bos taurus
O5i10	macaca fasc
O483y6	tetraodon n
P13590	gallus gall
Q5du03	mus musculus
O5r1q0	felle silve
O5g7g8	felle silve
Q24327	drosophila
P20241	drosophila
Q8i0l3	caenorhabdi
O76518	caenorhabdi
O811h7	mus musculus
O76697	caenorhabdi
Q699p0	antherea p
O61352	mus musculus
P13592	homo sapien
O59f17	homo sapien
P13591	homo sapien
Q25198	hydra atten
O86x47	homo sapien
O14631	homo sapien
Q4kgm0	homo sapien
O4rsg5	tetraodon n
Q486a5	tetraodon n
O6rwt4	bos taurus
Q6rwt5	bos taurus

251 151 9.4 1702 2 Q4RJ21_TETNG Q4rj21 tetraodon n
 252 151 9.4 1898 2 Q9EQ17_MOUSE Q9eq17 mus musculus
 253 151 9.4 10495 2 Q4RE92_TETNG Q4re92 tetraodon n
 254 150.5 9.4 296 2 Q42404_CHICK Q42404 gallus gall
 255 150.5 9.4 1051 1 PTK7_CHICK PTK7 gallus gall
 256 150.5 9.4 1199 2 Q21041_CAEBL Q21041 caenorhabdi
 257 150 9.3 372 2 Q6VAN6_BOVIN Q6van6 bos taurus
 258 150 9.3 429 2 Q6VAN7_BOVIN Q6van7 bos taurus
 259 150 9.3 433 2 Q9V644_DROME Q9v644 drosophila
 260 150 9.3 847 1 FSTL5_MOUSE FSTL5 mus musculus
 261 150 9.3 1280 2 Q4RRJ3_TETNG Q4rrj3 tetraodon n
 262 150 9.3 1501 2 Q9QW00_9MURI Q9qw00 rattus sp.
 263 150 9.3 1501 2 Q4JFL8_RAT Q4jfl8 rattus norv
 264 150 9.3 1863 2 Q64605_RAT Q64605 rattus norv
 265 150 9.3 1898 2 Q64604_RAT Q64604 rattus norv
 266 149.5 9.3 89 2 Q4TR25_TETNG Q4te25 tetraodon n
 267 149.5 9.3 349 1 CEAH8_HUMAN CEAH8 homo sapien
 268 149.5 9.3 372 2 Q8KLG0_RAT Q8klg0 rattus norv
 269 149.5 9.3 373 2 Q8R373_MOUSE Q8r373 mus musculus
 270 149.5 9.3 388 2 Q8R464_MOUSE Q8r464 mus musculus
 271 149.5 9.3 439 2 Q6RWT6_BOVIN Q6rwt6 bos taurus
 272 149.5 9.3 519 1 CEAH1_RAT CEAH1 rattus norv
 273 149.5 9.3 551 2 Q8NHN7_HUMAN Q8nhn7 rattus norv
 274 149.5 9.3 1033 2 Q9V643_DROME Q9v643 drosophila
 275 149.5 9.3 1264 2 P91767_MANSE P91767 manduca sex
 276 149.5 9.3 1406 2 Q9GPp7_DROME Q9gp7 drosophila
 277 149.5 9.3 1463 2 Q9V008_DROME Q9vq08 drosophila
 278 149.5 9.3 6620 2 Q96AA2_HUMAN Q96aa2 homo sapien
 279 149.5 9.3 6620 2 Q5VST9_HUMAN Q5vst9 homo sapien
 280 149 9.3 524 2 Q7PSJ8_ANOGA Q7psj8 anopheles g
 281 149 9.3 605 2 Q6GNL9_XENLA Q6gnl9 xenopus lae
 282 149 9.3 1277 1 L1CAM_FUGRU Q98902 fugu rubrip
 283 149 9.3 1497 2 Q5XJV4_MOUSE Q5xjv4 mus musculus
 284 149 9.3 1499 2 Q90815_CHICK Q90815 gallus gall
 285 149 9.3 1501 2 Q7TT17_MOUSE Q7tt17 mus musculus
 286 149 9.3 1904 2 Q64699_MOUSE Q64699 mus musculus
 287 149 9.3 1907 2 Q4JFC7_MOUSE Q4jfc7 mus musculus
 288 148.5 9.3 436 2 Q6VAN8_BOVIN Q6van8 bos taurus
 289 148.5 9.3 838 2 Q90YH1_BRARE Q90yh1 brachydanio
 290 148.5 9.3 1253 2 Q4SCT8_TETNG Q4sc8 tetraodon n
 291 148 9.2 359 1 LACH_DROME Q24372 drosophila
 292 148 9.2 838 2 Q8BQ96_MOUSE Q8bq96 mus musculus
 293 148 9.2 838 2 Q8C4B2_MOUSE Q8c4b2 mus musculus
 294 148 9.2 841 2 Q5STE3_MOUSE Q5ste3 mus musculus
 295 148 9.2 858 1 NCAM1_RAT P13596 rattus norv
 296 148 9.2 1070 2 Q4S2F2_TETNG Q4s2f2 tetraodon n
 297 148 9.2 1379 2 P79701_COTCO P79701 coturnix co
 298 148 9.2 1513 2 Q90270_BRARE Q90270 brachydanio
 299 147.5 9.2 275 2 Q8AVV1_XENLA Q8avv1 xenopus lae
 300 147.5 9.2 333 1 AMAL_DROME P15364 drosophila
 301 147.5 9.2 341 2 Q7KSX2_DROME Q7ksx2 drosophila
 302 147.5 9.2 389 2 Q5U3R8_BRARE Q5u3r8 brachydanio
 303 147.5 9.2 390 2 Q66KX2_XENLA Q66kx2 xenopus lae
 304 147.5 9.2 943 2 Q7PRK4_ANOGA Q7prk4 anopheles g
 305 147.5 9.2 1271 2 Q6U714_BRARE Q6u714 brachydanio
 306 147.5 9.2 1912 1 PTPRD_HUMAN P23468 homo sapien
 307 147.5 9.2 2057 2 Q4T2N4_TETNG Q4t2n4 tetraodon n
 308 147 9.2 323 2 Q7QBA7_ANOGA Q7qba7 anopheles g
 309 147 9.2 358 2 Q90490_BRARE Q90490 brachydanio
 310 147 9.2 406 2 Q8N7T8_HUMAN Q8n7t8 homo sapien
 311 147 9.2 454 2 Q91W54_MOUSE Q91w54 mus musculus
 312 147 9.2 525 2 Q5R9N6_PONPY Q5r9n6 pongo pygma
 313 147 9.2 725 2 Q5I2D5_CANFA Q5i2d5 canis fami
 314 147 9.2 847 2 Q5I2D7_CANFA Q5i2d7 canis fami
 315 147 9.2 857 2 Q5I2D6_CANFA Q5i2d6 canis fami
 316 147 9.2 4129 2 Q59E65_DROME Q59e65 drosophila
 317 146.5 9.1 409 2 Q4SFV2_TETNG Q4sfv2 tetraodon n
 318 146.5 9.1 508 1 FCRL2_HUMAN Q61a5 homo sapien
 319 146.5 9.1 549 2 Q9D006_MOUSE Q9d006 mus musculus
 320 146.5 9.1 904 2 Q7PME2_ANOGA Q7pme2 anopheles g
 321 146.5 9.1 1056 2 Q90203_XENLA Q90203 xenopus lae
 322 146.5 9.1 1093 1 LRIG1_HUMAN Q96ja1 homo sapien
 323 146.5 9.1 1093 2 Q5XWD3_HUMAN Q5xwd3 homo sapien

324 146.5 9.1 1612 1 ROBO1_MOUSE 1612
 325 146.5 9.1 1651 1 ROBO1_RAT 1651
 326 146 9.1 353 2 Q86XY3_HUMAN 353
 327 146 9.1 373 2 Q7KYP5_HUMAN 373
 328 146 9.1 434 2 Q6DN72_HUMAN 434
 329 146 9.1 464 2 Q16170_HUMAN 464
 330 146 9.1 468 2 Q96CA7_HUMAN 468
 331 146 9.1 526 1 CEAH1_HUMAN 526
 332 146 9.1 605 2 Q921P2_MOUSE Q921p2 mus musculus
 333 146 9.1 1479 2 Q7KQT5_DROME Q7kqt5 drosophila
 334 146 9.1 1482 2 Q9V4Y0_DROME Q9v4y0 drosophila
 335 146 9.1 1788 2 Q9IAJ0_XENLA Q9iaj0 xenopus lae
 336 145.5 9.1 373 2 Q920S5_MOUSE Q920s5 mus musculus
 337 145.5 9.1 807 2 Q5EA96_BOVIN Q5ea96 bos taurus
 338 145.5 9.1 1077 2 Q5WN88_CAEBR Q5wn88 caenorhabdi
 339 145.5 9.1 1340 2 Q5U176_DROME Q5u176 drosophila
 340 145.5 9.1 1651 1 ROBO1_HUMAN 1651
 341 145.5 9.1 1709 1 SN_HUMAN 1709
 342 145 9.0 764 1 ICCR_DROME 764
 343 145 9.0 853 1 NCAM1_BOVIN 853
 344 145 9.0 1028 2 Q6INB5_XENLA 1028
 345 145 9.0 1244 2 Q69YJ3_HUMAN 1244
 346 145 9.0 1250 2 Q88971_MOUSE 1250
 347 145 9.0 1357 2 Q5MD89_BRARE 1357
 348 145 9.0 1357 2 Q5GIT2_BRARE 1357
 349 145 9.0 1395 2 Q7KVK3_DROME 1395
 350 145 9.0 1395 2 Q44924_DROME 1395
 351 145 9.0 1429 2 Q9W213_DROME 1429
 352 145 9.0 1905 2 Q5VVL9_HUMAN 1905
 353 145 9.0 2673 2 Q96SC3_HUMAN 2673
 354 144.5 9.0 316 2 Q8WP58_DROS1 316
 355 144.5 9.0 316 2 Q8WP94_DROS1 316
 356 144.5 9.0 316 2 Q8WPB3_DROS1 316
 357 144.5 9.0 1048 2 Q7QH01_ANOGA 1048
 358 144.5 9.0 1060 2 Q9Q213_RAT 1060
 359 144.5 9.0 1102 2 Q923W7_MOUSE 1102
 360 144.5 9.0 1109 2 Q8CE91_MOUSE 1109
 361 144.5 9.0 1109 2 Q6P5H3_MOUSE 1109
 362 144.5 9.0 1109 2 Q6AZB0_MOUSE 1109
 363 144.5 9.0 1110 2 Q8CE73_MOUSE 1110
 364 144.5 9.0 1269 2 Q01632_CAEBL 1269
 365 144.5 9.0 1273 2 Q44928_CAEBL 1273
 366 144.5 9.0 1285 2 Q5TYT1_BRARE 1285
 367 144.5 9.0 1335 2 Q610C7_CAEBR 1335
 368 144.5 9.0 3707 1 PGBM_MOUSE 3707
 369 144.5 9.0 4463 2 Q8MLD8_DROME 4463
 370 144.5 9.0 9270 2 Q8MLD9_DROS1 9270
 371 144 9.0 292 2 Q4RFQ9_TETNG 292
 372 144 9.0 403 2 Q9VP08_DROME 403
 373 144 9.0 662 2 Q60926_HUMAN 662
 374 144 9.0 702 2 Q8N4D0_HUMAN 702
 375 144 9.0 725 1 NCA12_MOUSE 725
 376 144 9.0 764 2 Q8MQQ1_DROME 764
 377 144 9.0 764 2 Q9W4U1_DROME 764
 378 144 9.0 862 2 Q4SAP3_TETNG 862
 379 144 9.0 1115 1 NCA11_MOUSE 1115
 380 144 9.0 1502 2 Q9UM61_HUMAN 1502
 381 144 9.0 1614 2 Q8UVD7_XENLA 1614
 382 144 9.0 1827 2 Q9VSG5_DROME 1827
 383 144 9.0 2331 2 Q59EG0_HUMAN 2331
 384 144 9.0 3198 2 Q9UG88_MANSE 3198
 385 143.5 8.9 398 2 Q8N126_HUMAN 398
 386 143.5 8.9 432 2 Q9UJF1_HUMAN 432
 387 143.5 8.9 438 2 Q9JLB7_MOUSE 438
 388 143.5 8.9 458 2 Q61351_MOUSE 458
 389 143.5 8.9 484 2 Q6BR00_XENLA 484
 390 143.5 8.9 510 2 Q9JLB8_MOUSE 510
 391 143.5 8.9 549 2 Q9JLB9_MOUSE 549
 392 143.5 8.9 758 2 Q9N2H7_PIG 758
 393 143.5 8.9 1108 2 Q5RJH4_MOUSE 1108
 394 143.5 8.9 1268 2 Q619L9_CAEBR 1268
 395 143.5 8.9 1386 1 ROBO3_HUMAN 1386
 396 143.5 8.9 3410 2 Q7TN00_RAT 3410

397	143	8.9	202	2	Q9NBC1_DROME	Q9nbc1 drosophila	470	139.5	8.7	366	2	Q6NVZ3_HUMAN	Q6nvz3 homo sapien
398	143	8.9	213	2	Q9N167_PAPHA	Q9n167 papio hamad	471	139.5	8.7	1375	2	Q8ML47_DROME	Q8ml47 drosophila
399	143	8.9	231	2	Q9NBB9_DROME	Q9nbb9 drosophila	472	139.5	8.7	1389	2	Q90Z69_BRARE	Q90z69 brachydanio
400	143	8.9	413	2	Q6ZNI1_HUMAN	Q6znl1 homo sapien	473	139.5	8.7	1419	2	Q98SW3_BRARE	Q98sw3 brachydanio
401	143	8.9	418	2	Q501T5_BRARE	Q501t5 brachydanio	474	139.5	8.7	1526	2	Q9V6D5_DROME	Q9v6d5 drosophila
402	143	8.9	437	2	Q7QG58_ANOGA	Q7qg58 anopheles g	475	139.5	8.7	6710	2	Q61SF4_CAEBR	Q61sf4 caenorhabdi
403	143	8.9	702	1	CEAM5_HUMAN	P06731 homo sapien	476	139	8.7	324	2	Q7TMH2_MOUSE	Q7tmh2 mus musculus
404	143	8.9	702	2	Q53G30_HUMAN	Q53g30 homo sapien	477	139	8.7	332	1	CD22_PANPA	Q9n1e5 pan paniscu
405	143	8.9	1114	2	Q9BWW1_HUMAN	Q9bww1 homo sapien	478	139	8.7	332	1	CD22_PANTR	Q9n1e6 pan troglod
406	143	8.9	1115	2	Q6UXJ5_HUMAN	Q6uxj5 homo sapien	479	139	8.7	336	2	Q9D6E7_MOUSE	Q9d6e7 mus musculus
407	143	8.9	1239	2	Q61PF2_CAEBR	Q61pf2 caenorhabdi	480	139	8.7	336	2	Q8QVG4_MOUSE	Q8qvg4 mus musculus
408	142.5	8.9	236	2	Q4T419_TETNG	Q4t419 tetraodon n	481	139	8.7	343	2	Q8R4Y0_MOUSE	Q8r4y0 mus musculus
409	142.5	8.9	265	1	CEAM7_HUMAN	Q14002 homo sapien	482	139	8.7	399	2	Q8N772_HUMAN	Q8n772 homo sapien
410	142.5	8.9	601	2	Q96CJ3_HUMAN	Q96cj3 homo sapien	483	139	8.7	434	2	Q4RFG0_TETNG	Q4rfg0 tetraodon n
411	142.5	8.9	931	2	Q8KAM5_MOUSE	Q8kam5 mus musculus	484	139	8.7	477	2	Q5VNE5_HUMAN	Q5vne5 homo sapien
412	142.5	8.9	1019	2	Q8XJK6_MOUSE	Q8xjk6 mus musculus	485	139	8.7	537	2	Q5VTD4_HUMAN	Q5vtd4 homo sapien
413	142.5	8.9	1256	1	Q35158_RAT	Q35158 rattus norv	486	139	8.7	553	2	Q8WXJ5_HUMAN	Q8wxj5 homo sapien
414	142.5	8.9	1894	1	PTPRD_MOUSE	Q64487 mus musculus	487	139	8.7	602	2	Q86YJ9_HUMAN	Q86yj9 homo sapien
415	142.5	8.9	1948	1	PTPRS_HUMAN	Q13332 homo sapien	488	139	8.7	646	2	Q8NHN8_HUMAN	Q8nhn8 homo sapien
416	142.5	8.9	3165	2	Q7Q767_ANOGA	Q7q767 anopheles g	489	139	8.7	650	2	Q8NAB4_HUMAN	Q8nab4 homo sapien
417	142	8.8	292	2	Q6UY47_HUMAN	Q6uy47 homo sapien	490	139	8.7	781	2	Q5SGJ1_HUMAN	Q5sgj1 homo sapien
418	142	8.8	335	2	Q5XKA0_XENLA	Q5xka0 xenopus lae	491	139	8.7	822	1	NTRK2_HUMAN	Q5vvp4 homo sapien
419	142	8.8	335	2	Q6XRC3_HUMAN	Q6xrc3 homo sapien	492	139	8.7	822	1	Q5VVP4_HUMAN	Q5vvp4 homo sapien
420	142	8.8	458	2	Q63093_RAT	Q63093 rattus norv	493	139	8.7	838	2	Q8WXJ7_HUMAN	Q8wxj7 homo sapien
421	142	8.8	532	2	Q6NNU3_DROME	Q6nnu3 drosophila	494	139	8.7	1225	2	Q6GP61_XENLA	Q6gp61 xenopus lae
422	142	8.8	740	2	Q96P29_HUMAN	Q96p29 homo sapien	495	139	8.7	1348	2	Q677M1_CHICK	Q677m1 gallus gall
423	142	8.8	847	1	CD22_HUMAN	F20273 homo sapien	496	139	8.7	1759	2	Q7P8H8_ANOGA	Q7p8h8 anopheles g
424	142	8.8	1237	2	Q61OC8_CAEBR	Q61oc8 caenorhabdi	497	138.5	8.6	278	2	Q9QLJ3_MOUSE	Q9qlj3 mus musculus
425	142	8.8	1560	2	Q59FX6_HUMAN	Q59fx6 homo sapien	498	138.5	8.6	330	2	Q90Z42_CHICK	Q90z42 gallus gall
426	142	8.8	1730	2	Q7YRQ7_PIG	Q7yrq7 sus scrofa	499	138.5	8.6	344	1	NTRI_MOUSE	Q9p9j0 mus musculus
427	141.5	8.8	312	2	Q66KV0_XENLA	Q66kv0 xenopus lae	500	138.5	8.6	344	2	Q8BG33_MOUSE	Q8bg33 m mus muscu
428	141.5	8.8	344	1	NTRI_RAT	Q62718 rattus norv	501	138.5	8.6	508	2	Q8CED8_MOUSE	Q8ced8 mus musculus
429	141.5	8.8	405	2	Q7PRJ5_ANOGA	Q7prj5 anopheles g	502	138.5	8.6	1375	2	Q94537_DROME	Q94537 drosophila
430	141.5	8.8	483	2	Q9DBP8_MOUSE	Q9dbp8 mus musculus	503	138.5	8.6	1526	2	Q94538_DROME	Q94538 drosophila
431	141.5	8.8	508	2	Q8R007_MOUSE	Q8r007 mus musculus	504	138	8.6	283	2	Q7PCU3_ANOGA	Q7pcu3 anopheles g
432	141.5	8.8	509	2	Q9EOY5_MOUSE	Q9egy5 m mman-g pr	505	138	8.6	283	2	Q5TNQ2_ANOGA	Q5tnq2 anopheles g
433	141.5	8.8	635	2	Q4S188_TETNG	Q4s188 tetraodon n	506	138	8.6	379	1	JAML1_MOUSE	Q8n0l9 mus musculus
434	141.5	8.8	1937	2	Q7QT88_ANOGA	Q7qt88 anopheles g	507	138	8.6	510	2	Q5E9Z9_BOVIN	Q5e9z9 bos taurus
435	141	8.8	154	2	Q7PSN2_ANOGA	Q7psn2 anopheles g	508	138	8.6	796	2	Q91287_PLEWA	Q91287 pleurodeles
436	141	8.8	218	2	Q7PJ18_ANOGA	Q7pj18 anopheles g	509	138	8.6	804	2	Q800Z1_BRARE	Q800z1 brachydanio
437	141	8.8	296	2	Q29890_HUMAN	Q29890 homo sapien	510	138	8.6	806	2	Q90Z00_BRARE	Q90z00 brachydanio
438	141	8.8	333	2	Q86WB8_HUMAN	Q86wb8 homo sapien	511	138	8.6	2772	2	Q9VAV4_DROME	Q9vav4 drosophila
439	141	8.8	529	2	Q4SMH3_TETNG	Q4smh3 tetraodon n	512	138	8.6	2894	2	Q7KRX2_DROME	Q7krx2 drosophila
440	141	8.8	532	2	Q9VLF0_DROME	Q9vlf0 drosophila	513	137.5	8.6	282	2	Q9Y639_HUMAN	Q9y639 homo sapien
441	141	8.8	862	1	CD22_MOUSE	F35329 mus musculus	514	137.5	8.6	416	2	Q8N713_HUMAN	Q8n713 homo sapien
442	141	8.8	955	2	Q8MQ86_CAEBL	Q8mq86 caenorhabdi	515	137.5	8.6	509	2	Q91YK7_MOUSE	Q91y7 mus musculus
443	141	8.8	1150	2	Q4SL82_TETNG	Q4sl82 tetraodon n	516	137.5	8.6	528	2	P91670_DROME	P91670 drosophila
444	141	8.8	1278	2	Q4RR55_TETNG	Q4rra5 tetraodon n	517	137.5	8.6	536	2	Q4V5E0_DROME	Q4v5e0 drosophila
445	141	8.8	2016	2	Q9NBA1_DROME	Q9nba1 drosophila	518	137.5	8.6	545	2	Q9VCT4_DROME	Q9vct4 drosophila
446	141	8.8	2051	2	Q43328_HIRME	Q43328 hirudo medi	519	137.5	8.6	549	2	Q9NQS3_HUMAN	Q9nqs3 homo sapien
447	141	8.8	2234	2	Q4SLN7_TETNG	Q4sln7 tetraodon n	520	137.5	8.6	551	2	Q8MSN7_DROME	Q8msn7 drosophila
448	140.5	8.8	542	2	Q5USW7_MOUSE	Q5usw7 mus musculus	521	137.5	8.6	606	2	Q9VNM6_DROME	Q9vnm6 drosophila
449	140.5	8.8	632	2	Q2RKS5_HUMAN	Q2rks5 homo sapien	522	137.5	8.6	709	2	Q8IXC7_HUMAN	Q8ixc7 homo sapien
450	140.5	8.8	810	2	Q9PS96_XENLA	Q9ps96 xenopus lae	523	137.5	8.6	800	2	Q9JHX9_RAT	Q9jhx9 rattus norv
451	140.5	8.8	931	2	Q8NF26_HUMAN	Q8nf26 homo sapien	524	137.5	8.6	800	2	Q86LF8_DROVI	Q86lf8 drosophila
452	140.5	8.8	946	2	Q07153_TORCA	Q07153 torpedo cal	525	137.5	8.6	801	2	Q86LF8_DROVI	Q86lf8 drosophila
453	140.5	8.8	1062	2	Q8BKG3_MOUSE	Q8bk93 mus musculus	526	137.5	8.6	956	2	Q9W4T9_DROME	Q9w4t9 drosophila
454	140.5	8.8	1994	2	Q6ZPP2_MOUSE	Q6zpp2 mus musculus	527	137.5	8.6	959	2	Q9N9Y9_DROME	Q9n9y9 drosophila
455	140.5	8.8	2176	2	Q6V4S5_MOUSE	Q6v4s5 mus musculus	528	137.5	8.6	975	2	Q97174_DROME	Q97174 drosophila
456	140.5	8.8	2623	2	Q6WR10_HUMAN	Q6wr10 homo sapien	529	137.5	8.6	1000	2	Q4TBR4_TETNG	Q4tbr4 tetraodon n
457	140	8.7	340	2	Q61349_MOUSE	Q61349 mus musculus	530	137.5	8.6	1249	2	Q7TMZ9_RAT	Q7tmz9 rattus norv
458	140	8.7	381	2	Q9Y4A4_HUMAN	Q9y4a4 homo sapien	531	137.5	8.6	1249	2	Q90933_CHICK	Q90933 gallus gall
459	140	8.7	420	2	Q68DM9_HUMAN	Q68dm9 homo sapien	532	137.5	8.6	1466	2	Q68U72_APIME	Q68u72 apis mellif
460	140	8.7	437	2	Q8NFE5_HUMAN	Q8nfe5 homo sapien	533	137.5	8.6	7105	2	Q7PXW9_ANOGA	Q7pxw9 anopheles g
461	140	8.7	591	2	Q6NP04_DROME	Q6np04 drosophila	534	137	8.5	267	2	Q8NC05_HUMAN	Q8nc05 homo sapien
462	140	8.7	977	2	Q96RD9_HUMAN	Q96rd9 homo sapien	535	137	8.5	391	2	Q4S871_TETNG	Q4s871 tetraodon n
463	140	8.7	977	2	Q5VYK9_HUMAN	Q5vyk9 homo sapien	536	137	8.5	474	2	Q5FV48_FUGRU	Q5fv48 fugu rubrip
464	140	8.7	1261	2	Q4JFL6_RAT	Q4jfl6 rattus norv	537	137	8.5	526	1	BTIA1_BOVIN	BTia1 bos taurus
465	140	8.7	1495	2	Q4JFL7_RAT	Q4jfl7 rattus norv	538	137	8.5	570	2	Q8NCE6_HUMAN	Q8nce6 homo sapien
466	140	8.7	2016	2	Q8MKM6_DROME	Q8mk6 drosophila	539	137	8.5	619	2	Q7PX10_ANOGA	Q7px10 anopheles g
467	140	8.7	2016	2	Q8MKM7_DROME	Q8mk7 drosophila	540	137	8.5	784	2	Q81063_DROVI	Q81063 drosophila
468	140	8.7	2019	2	Q8MKM8_DROME	Q8mk8 drosophila	541	137	8.5	913	2	Q8T3E5_CABEL	Q8t3e5 caenorhabdi
469	140	8.7	2022	2	Q7KQK5_DROME	Q7kqk5 drosophila	542	137	8.5	928	2	Q19128_CABEL	Q19128 caenorhabdi

543	137	8.5	1164	2	Q66MN5_DROVI	Q66mn5 drosophila	616	133.5	8.3	4098	2	Q7PQ39_ANOGA	Q7pq39 anopheles g
544	137	8.5	1249	2	Q90Z04_XENLA	Q90z04 xenopus lae	617	133	8.3	289	2	Q9QYL5_MOUSE	Q9qyl5 mus musculus
545	137	8.5	1272	2	Q5G1T3_BRARE	Q5g1t3 brachydanio	618	133	8.3	305	2	Q6P3A4_MOUSE	Q6p3a4 mus musculus
546	137	8.5	1366	1	ROBO3_MOUSE	Q92214 mus musculus	619	133	8.3	311	2	Q6DN73_HUMAN	Q6dn73 homo sapien
547	137	8.5	1367	2	Q7PQF4_ANOGA	Q7pqf4 anopheles g	620	133	8.3	334	2	Q02870_CHICK	Q02870 gallus gall
548	136.5	8.5	375	2	Q4S919_TETNG	Q4s919 tetraodon n	621	133	8.3	338	1	Q62813_rattus norv	Q62813 rattus norv
549	136.5	8.5	393	2	P97547_RAT	P97547 rattus norv	622	133	8.3	338	1	LSAMP_RAT	LSAMP_RAT
550	136.5	8.5	394	2	Q72XX1_XENLA	Q72xx1 xenopus lae	623	133	8.3	377	2	Q4RZV7_TETNG	Q4rzv7 tetraodon n
551	136.5	8.5	459	2	Q4RS41_TETNG	Q4rs41 tetraodon n	624	133	8.3	459	2	Q9JHL6_RAT	Q9jhl6 rattus norv
552	136.5	8.5	821	1	NTRK2_MOUSE	P15209 mus musculus	625	133	8.3	639	2	Q96P30_HUMAN	Q96p30 homo sapien
553	136.5	8.5	1328	2	Q4RKW3_TETNG	Q4rkW3 tetraodon n	626	133	8.3	707	2	Q5VXZ8_HUMAN	Q5vxz8 homo sapien
554	136	8.5	416	2	Q67IP8_HUMAN	Q67ip8 homo sapien	627	133	8.3	734	2	Q96LA4_HUMAN	Q96la4 homo sapien
555	136	8.5	500	1	BTNL8_HUMAN	Q6ux41 homo sapien	628	133	8.3	734	2	Q96P31_HUMAN	Q96p31 homo sapien
556	136	8.5	941	2	Q4SMD8_TETNG	Q4smD8 tetraodon n	629	133	8.3	742	2	Q8N6S2_HUMAN	Q8n6s2 homo sapien
557	136	8.5	1270	2	Q9U3P2_CAERL	Q9u3p2 caenorhabdi	630	133	8.3	919	1	UNC5_CAERL	UNC5_CAERL
558	136	8.5	1478	2	Q59H90_HUMAN	Q59h90 homo sapien	631	133	8.3	955	1	MDGA1_HUMAN	MDGA1_HUMAN
559	136	8.5	1906	1	MYLK_CHICK	P11799 gallus gall	632	133	8.3	1065	1	LRIQZ2_HUMAN	LRIQZ2_HUMAN
560	135.5	8.4	326	2	Q9N166_PAPHA	Q9n166 papio hamad	633	133	8.3	1177	2	Q6GQB1_XENLA	Q6gqb1 xenopus lae
561	135.5	8.4	484	2	Q5QSL1_XENTR	Q5qsl1 xenopus tro	634	133	8.3	2213	2	Q7Z5N4_HUMAN	Q7z5n4 homo sapien
562	135.5	8.4	563	2	Q5PWR8_XENTR	Q5fwr8 xenopus tro	635	132.5	8.3	309	2	Q91YV7_MOUSE	Q91yv7 mus musculus
563	135.5	8.4	881	2	Q60UL6_CAERL	Q60ul6 caenorhabdi	636	132.5	8.3	312	2	Q4SNG2_TETNG	Q4sng2 tetraodon n
564	135.5	8.4	1010	1	CNTN1_CHICK	P14781 gallus gall	637	132.5	8.3	337	2	Q6GLZ7_XENLA	Q6glz7 xenopus lae
565	135.5	8.4	1030	2	Q8NFA8_HUMAN	Q8nfa8 homo sapien	638	132.5	8.3	398	2	Q9Y640_HUMAN	Q9y640 homo sapien
566	135.5	8.4	1227	2	Q21038_CAERL	Q21038 caenorhabdi	639	132.5	8.3	416	2	Q7Q1Z7_ANOGA	Q7q1z7 anopheles g
567	135.5	8.4	1843	2	Q4SPF7_TETNG	Q4spf7 tetraodon n	640	132.5	8.3	448	2	Q9JHL7_RAT	Q9jhl7 rattus norv
568	135.5	8.4	2293	2	Q4T1M4_TETNG	Q4tlm4 tetraodon n	641	132.5	8.3	800	2	Q99052_MOUSE	Q99052 mus musculus
569	135	8.4	238	2	Q5YJ11_SHEEP	Q5yjl1 ovis aries	642	132.5	8.3	800	2	Q7TS18_MOUSE	Q7ts18 mus musculus
570	135	8.4	277	2	Q61R88_RAT	Q61r88 rattus norv	643	132.5	8.3	801	1	FGPR3_MOUSE	FGPR3_MOUSE
571	135	8.4	281	2	P97546_RAT	P97546 rattus norv	644	132.5	8.3	814	1	PUNC_HUMAN	PUNC_HUMAN
572	135	8.4	281	2	P97300_MOUSE	P97300 mus musculus	645	132.5	8.3	920	1	Q4RSG7_TETNG	Q4rsg7 tetraodon n
573	135	8.4	302	2	Q5YJ10_SHEEP	Q5yji10 ovis aries	646	132.5	8.3	949	1	Q4SL83_TETNG	Q4sl83 tetraodon n
574	135	8.4	337	1	OCBM_CHICK	Q98892 gallus gall	647	132.5	8.3	1099	1	CNTN5_RAT	P97527 rattus norv
575	135	8.4	338	1	LSAMP_HUMAN	Q13449 homo sapien	648	132.5	8.3	1133	2	Q4T6R5_TETNG	Q4t6r5 tetraodon n
576	135	8.4	344	2	Q9DF61_CHICK	Q9df61 gallus gall	649	132.5	8.3	1209	2	Q4SFS8_TETNG	Q4sfs8 tetraodon n
577	135	8.4	367	2	Q6ZW14_HUMAN	Q6zw14 homo sapien	650	132.5	8.3	1304	2	Q9VBE5_DROME	Q9vbe5 drosophila
578	135	8.4	461	2	Q13854_HUMAN	Q13854 homo sapien	651	132.5	8.3	1356	1	VGFR2_HUMAN	P359e80 homo sapien
579	135	8.4	1379	2	Q4SMF3_TETNG	Q4smf3 tetraodon n	652	132.5	8.3	1451	2	Q59EB0_HUMAN	Q59eb0 mus musculus
580	135	8.4	2776	2	Q869A0_DROME	Q869a0 drosophila	653	132	8.2	510	2	Q6EH12_RAT	Q6eh12 rattus norv
581	135	8.4	2898	2	Q868Z9_DROME	Q868z9 drosophila	654	132	8.2	1070	1	PTK7_HUMAN	Q13308 homo sapien
582	134.5	8.4	214	2	Q4SX01_TETNG	Q4sx01 tetraodon n	655	132	8.2	1092	2	Q91ZT0_RAT	Q91zt0 rattus norv
583	134.5	8.4	290	1	PD11_HUMAN	Q9nzq7 homo sapien	656	132	8.2	1272	2	Q4JDD5_BRARE	Q4jdds brachydanio
584	134.5	8.4	316	2	Q7TPB4_RAT	Q7tpb4 rattus norv	657	132	8.2	1333	1	VGFR1_MOUSE	P35969 mus musculus
585	134.5	8.4	322	1	ICOSL_MOUSE	Q9jh18 mus musculus	658	132	8.2	1348	1	VGPR2_COTJA	P52583 coturnix co
586	134.5	8.4	322	2	Q544C7_MOUSE	Q544c7 mus musculus	659	132	8.2	1363	2	Q91ZT1_RAT	Q91zt1 rattus norv
587	134.5	8.4	368	2	Q5ZJK6_CHICK	Q5zjk6 gallus gall	660	132	8.2	1561	2	Q924D2_MOUSE	Q924d2 mus musculus
588	134.5	8.4	676	2	Q4SIF9_TETNG	Q4sif9 tetraodon n	661	132	8.2	1949	2	Q6PDN3_MOUSE	Q6pdn3 mus musculus
589	134.5	8.4	677	2	Q7PWJ1_ANOGA	Q7pwj1 anopheles g	662	132	8.2	2024	2	Q53CM6_BRARE	Q53cm6 brachydanio
590	134.5	8.4	761	2	Q95LQ2_MACFA	Q95lq2 macaca fasc	663	132	8.2	2222	2	Q4RY92_TETNG	Q4ry92 tetraodon n
591	134.5	8.4	814	2	Q91897_XENLA	Q91897 xenopus lae	664	132	8.2	4736	2	Q7YT99_MYTGA	Q7yt99 mytilus gal
592	134.5	8.4	821	1	NTRK2_RAT	Q83604 rattus norv	665	131.5	8.2	175	2	Q4TCY2_TETNG	Q4tcy2 tetraodon n
593	134.5	8.4	1028	1	CNTN3_MOUSE	Q7409 mus musculus	666	131.5	8.2	226	2	Q7PUJ2_ANOGA	Q7puj2 anopheles g
594	134.5	8.4	1336	1	VGFR1_RAT	P53767 rattus norv	667	131.5	8.2	306	2	Q9R1Z9_MOUSE	Q9r1z9 mus musculus
595	134	8.3	277	2	Q8C6H8_MOUSE	Q8c6h8 mus musculus	668	131.5	8.2	309	1	CD86_MOUSE	P42082 mus musculus
596	134	8.3	343	2	Q8BY94_MOUSE	Q8by94 mus musculus	669	131.5	8.2	309	2	Q549Q9_MOUSE	Q549q9 mus musculus
597	134	8.3	698	2	Q5TN75_ANOGA	Q5tn75 anopheles g	670	131.5	8.2	314	2	Q61238_MOUSE	Q61238 mus musculus
598	134	8.3	747	2	Q5DT24_MOUSE	Q5dt24 mus musculus	671	131.5	8.2	344	1	NTRI_HUMAN	Q9p121 homo sapien
599	134	8.3	778	1	KIR3_MOUSE	Q8br86 mus musculus	672	131.5	8.2	344	2	Q5R554_PONPY	Q5r554 pongo pygma
600	134	8.3	868	1	MUSK_RAT	Q62838 rattus norv	673	131.5	8.2	356	2	Q64381_MOUSE	Q64381 mus musculus
601	134	8.3	954	2	Q9UL17_HUMAN	Q9ul17 anopheles g	674	131.5	8.2	538	2	Q28939_PIG	Q28939 sus scrofa
602	134	8.3	1023	2	Q9UL17_HUMAN	Q9ul17 homo sapien	675	131.5	8.2	606	2	Q4IRH8_RAT	Q4irh8 rattus norv
603	134	8.3	5505	2	Q4RU89_TETNG	Q4ru89 tetraodon n	676	131.5	8.2	747	2	Q4H3K6_CIOIN	Q4h3k6 ciona intes
604	133.5	8.3	265	2	Q8IPG9_DROME	Q8ipg9 drosophila	677	131.5	8.2	778	1	KIRB3_HUMAN	Q8iz90 homo sapien
605	133.5	8.3	298	2	Q96114_DROME	Q96114 drosophila	678	131.5	8.2	786	2	Q4SR20_TETNG	Q4sr20 tetraodon n
606	133.5	8.3	348	2	Q00557_HUMAN	Q00557 homo sapien	679	131.5	8.2	900	2	Q4SR23_TETNG	Q4sr23 tetraodon n
607	133.5	8.3	606	2	Q9ES8_RAT	Q9es88 rattus norv	680	131.5	8.2	1006	2	Q6IDE9_DROME	Q6ide9 drosophila
608	133.5	8.3	648	2	Q9EP22_RAT	Q9epf2 rattus norv	681	131.5	8.2	1140	2	Q4RRD1_TETNG	Q4rrd1 tetraodon n
609	133.5	8.3	812	1	FGFR1_XENLA	P22182 xenopus lae	682	131.5	8.2	1387	2	Q4SUQ3_TETNG	Q4suj3 tetraodon n
610	133.5	8.3	816	2	Q8NFA5_HUMAN	Q8nfa5 homo sapien	683	131	8.2	295	2	Q9QYL6_MOUSE	Q9qyl6 mus musculus
611	133.5	8.3	948	2	Q9VME2_DROME	Q9vme2 drosophila	684	131	8.2	366	2	Q8N759_HUMAN	Q8n759 homo sapien
612	133.5	8.3	1070	2	Q6IQ54_HUMAN	Q6iq54 homo sapien	685	131	8.2	413	2	Q64OR3_MOUSE	Q64or3 mus musculus
613	133.5	8.3	1070	2	Q5T650_HUMAN	Q5t650 homo sapien	686	131	8.2	554	2	Q9W4R3_DROME	Q9w4r3 drosophila
614	133.5	8.3	1427	2	Q91562_XENLA	Q91562 xenopus lae	687	131	8.2	771	1	PIGR_MOUSE	Q70570 mus musculus
615	133.5	8.3	4071	2	Q7PH68_ANOGA	Q7ph68 anopheles g	688	131	8.2	817	2	Q4H2M8_CIOIN	Q4h2m8 ciona intes

689	131	8.2	1036	1	CNTN2_CHICK	P28685 gallus gall	762	139	8.0	1535	2	Q23991_DROME	Q23991 drosophila
690	131	8.2	1043	2	Q6PA07_XENLA	Q6pa07 xenopus lae	763	139	8.0	6048	2	Q7JN85_CABEL	Q7jn85 caenorhabdi
691	131	8.2	1252	2	Q9JUL1_MOUSE	Q9jul1 mus musculus	764	139	8.0	6839	2	Q23550_CABEL	Q23550 caenorhabdi
692	131	8.2	1428	2	Q8AY67_BRARE	Q8ay67 brachydanio	765	139	8.0	7158	2	Q23551_CABEL	Q23551 caenorhabdi
693	131	8.2	1896	2	Q9IAJ1_XENLA	Q9iaj1 xenopus lae	766	139	8.0	17352	2	Q89YM2_PROCL	Q89ym2 procambarus
694	130.5	8.1	91	2	Q91667_XENLA	Q91667 xenopus lae	767	128.5	8.0	272	2	Q8RIN5_MOUSE	Q8rin5 mus musculus
695	130.5	8.1	183	2	Q8NH6_HUMAN	Q8nh6 homo sapien	768	128.5	8.0	274	2	Q4W5Q0_HUMAN	Q4w5q0 homo sapien
696	130.5	8.1	208	2	Q8UN3_MOUSE	Q8unw3 mus musculus	769	128.5	8.0	294	2	Q8WE8_HUMAN	Q8we8 homo sapien
697	130.5	8.1	282	2	Q6UXZ0_HUMAN	Q6uxz0 homo sapien	770	128.5	8.0	325	2	Q501V7_BRARE	Q501v7 brachydanio
698	130.5	8.1	292	2	Q5HZR6_XENLA	Q5hzr6 xenopus lae	771	128.5	8.0	360	2	Q8MRE6_DROME	Q8mre6 drosophila
699	130.5	8.1	300	2	Q68SP0_MOUSE	Q68sp0 mus musculus	772	128.5	8.0	480	2	Q8PSC9_9PIPI	Q8psc9 xenopus. fi
700	130.5	8.1	316	2	Q5F3J1_CHICK	Q5f3j1 gallus gall	773	128.5	8.0	510	2	Q7L3E0_HUMAN	Q7l3e0 homo sapien
701	130.5	8.1	349	2	Q7QJG1_ANOGA	Q7qjg1 anopheles g	774	128.5	8.0	719	2	Q7U4G1_DROME	Q7u4g1 drosophila
702	130.5	8.1	428	2	Q66JG6_HUMAN	Q66jg6 homo sapien	775	128.5	8.0	757	1	PIGR_BOVIN	P1g265 bos taurus
703	130.5	8.1	429	2	Q96LA6_HUMAN	Q96la6 homo sapien	776	128.5	8.0	764	2	Q5RDC2_PONPY	Q5rdc2 pongo pygma
704	130.5	8.1	442	2	Q8C306_MOUSE	Q8c306 mus musculus	777	128.5	8.0	764	2	Q5R3A8_PONPY	Q5r3a8 pongo pygma
705	130.5	8.1	484	2	Q26475_SCHAM	Q26475 schistocerc	778	128.5	8.0	772	2	Q9Y2J6_HUMAN	Q9y2j6 homo sapien
706	130.5	8.1	487	1	FGRL1_CHICK	Q7t2h2 gallus gall	779	128.5	8.0	793	2	Q4RFN0_TETNG	Q4rfn0 tetraodon n
707	130.5	8.1	492	2	Q9ET54_MOUSE	Q9et54 mus musculus	780	128.5	8.0	814	2	Q6GNP8_XENLA	Q6gnp8 xenopus lae
708	130.5	8.1	538	2	Q29123_PIG	Q29123 sus scrofa	781	128.5	8.0	937	2	Q5WN68_CAEBR	Q5wn68 caenorhabdi
709	130.5	8.1	807	2	Q6NT23_BRARE	Q6ny23 brachydanio	782	128.5	8.0	1056	1	CNTN5_ERARE	Q7z34 brachydanio
710	130.5	8.1	853	2	Q6DFX7_MOUSE	Q6dfx7 mus musculus	783	128.5	8.0	1098	2	Q4RR11_TETNG	Q4rrt1 tetraodon n
711	130.5	8.1	940	2	Q8NFA7_HUMAN	Q8nfa7 homo sapien	784	128.5	8.0	1106	2	Q8WX93_HUMAN	Q8wx93 homo sapien
712	130.5	8.1	1015	2	Q4SNF9_TETNG	Q4snf9 tetraodon n	785	128.5	8.0	1914	1	MYLK_HUMAN	Q15746 homo sapien
713	130.5	8.1	1081	2	Q692T7_MOUSE	Q692t7 mus musculus	786	128.5	8.0	2016	2	Q86BQ7_DROME	Q86bq7 drosophila
714	130.5	8.1	1098	1	CNTN5_MOUSE	P68500 mus musculus	787	128.5	8.0	2224	2	Q7U1M1_DROME	Q7u1m1 drosophila
715	130.5	8.1	1192	2	Q610E4_CAEBR	Q610e4 caenorhabdi	788	128.5	8.0	2752	2	Q7QKD0_ANOGA	Q7qkd0 anopheles g
716	130.5	8.1	2174	2	Q9GQRO_DROME	Q9gqro drosophila	789	128.5	8.0	4447	2	Q8MXD8_CABEL	Q8mxd8 caenorhabdi
717	130.5	8.1	2217	2	Q8AV57_CHICK	Q8av57 gallus gall	790	128	8.0	403	2	Q6NZV3_BRARE	Q6nzv3 brachydanio
718	130	8.1	303	2	Q7ZXR4_XENLA	Q7zxr4 xenopus lae	791	128	8.0	411	2	Q7QGM5_ANOGA	Q7qgm5 anopheles g
719	130	8.1	320	2	Q4V828_XENLA	Q4v828 xenopus lae	792	128	8.0	506	1	SHP51_BOVIN	Q46631 bos taurus
720	130	8.1	321	2	Q6INP0_XENLA	Q6inf0 xenopus lae	793	128	8.0	507	2	Q5K4Q3_PIG	Q5k4q3 sus scrofa
721	130	8.1	341	1	LSAMP_MOUSE	Q8b1k3 mus musculus	794	128	8.0	531	2	Q7QRY7_ANOGA	Q7qry7 anopheles g
722	130	8.1	458	2	Q7PW77_ANOGA	Q7pw77 anopheles g	795	128	8.0	714	2	Q4T313_TETNG	Q4t313 tetraodon n
723	130	8.1	802	2	Q95M13_BOVIN	Q95ml3 bos taurus	796	128	8.0	869	1	MUSK_HUMAN	Q15146 homo sapien
724	130	8.1	885	2	Q8HYV1_PIG	Q8hyv1 sus scrofa	797	128	8.0	1180	2	Q5IS85_9PRIM	Q5is85 salmtri bol
725	130	8.1	886	2	Q8HYV2_PIG	Q8hyv2 sus scrofa	798	128	8.0	1363	1	VGPR3_MOUSE	P35917 mus musculus
726	130	8.1	912	2	Q4S2G4_TETNG	Q4s2g4 tetraodon n	799	128	8.0	1363	2	Q5SU91_MOUSE	Q5su91 mus musculus
727	130	8.1	1198	2	Q7QD44_ANOGA	Q7qdd4 anopheles g	800	128	8.0	1409	2	Q801M2_BRARE	Q801m2 brachydanio
728	129.5	8.1	232	2	Q9N168_PAPHA	Q9n168 papio hamad	801	128	8.0	1409	2	Q8J127_BRARE	Q8j127 brachydanio
729	129.5	8.1	345	2	Q58DA5_BOVIN	Q58da5 bos taurus	802	128	8.0	2095	2	Q4S8U5_TETNG	Q4s8u5 tetraodon n
730	129.5	8.1	361	2	Q5M960_RAT	Q5m960 rattus norv	803	128	8.0	4648	2	Q4T3W5_TETNG	Q4t3w5 tetraodon n
731	129.5	8.1	661	2	Q5RJM1_MOUSE	Q5rjw1 mus musculus	804	127.5	7.9	249	2	Q58DG9_BOVIN	Q58dg9 bos taurus
732	129.5	8.1	813	1	PUNC_MOUSE	Q8bqc3 mus musculus	805	127.5	7.9	316	2	Q8VE98_MOUSE	Q8ve98 mus musculus
733	129.5	8.1	1020	2	Q8NHNO_HUMAN	Q8nhno homo sapien	806	127.5	7.9	305	2	Q8VE98_MOUSE	Q8ve98 mus musculus
734	129.5	8.1	1095	2	Q58EP4_BRARE	Q58ep4 brachydanio	807	127.5	7.9	947	1	MUSK_CHICK	Q8axy6 gallus gall
735	129.5	8.1	1117	1	LRIG3_MOUSE	Q6pic6 mus musculus	808	127.5	7.9	1232	2	Q90284_CARAU	Q90284 carassius a
736	129	8.0	276	2	Q922H8_MOUSE	Q922h8 mus musculus	809	127.5	7.9	1238	2	Q58QC3_XENLA	Q58qc3 xenopus lae
737	129	8.0	295	2	Q922H8_MOUSE	Q922h8 mus musculus	810	127.5	7.9	1845	2	Q5MYA0_HUMAN	Q5mya0 homo sapien
738	129	8.0	308	2	Q503N7_BRARE	Q503n7 brachydanio	811	127.5	7.9	1914	2	Q5MY99_HUMAN	Q5my99 homo sapien
739	129	8.0	338	2	Q6DHD4_BRARE	Q6dhd4 brachydanio	812	127.5	7.9	1914	2	Q724J0_HUMAN	Q724j0 homo sapien
740	129	8.0	343	2	Q4SDU6_TETNG	Q4sdue6 tetraodon n	813	127.5	7.9	2169	2	Q8AV58_CHICK	Q8av58 gallus gall
741	129	8.0	350	2	Q02869_CHICK	Q02869 gallus gall	814	127	7.9	204	2	Q7FJY5_ANOGA	Q7fjy5 anopheles g
742	129	8.0	448	2	Q8IGAS_DROME	Q8iga5 drosophila	815	127	7.9	349	1	LACH_SCHAM	Q26474 schistocerc
743	129	8.0	537	2	Q7QSV8_ANOGA	Q7qsy8 anopheles g	816	127	7.9	504	1	FGRL1_HUMAN	Q8n441 m mus muscu
744	129	8.0	577	2	Q80Y42_MOUSE	Q80y42 mus musculus	817	127	7.9	577	2	Q9D2Z1_MOUSE	Q9d2z1 m mus muscu
745	129	8.0	650	2	Q9GKR2_BOVIN	Q9gkr2 bos taurus	818	127	7.9	782	2	Q61563_MOUSE	Q61563 mus musculus
746	129	8.0	700	1	KIRR2_MOUSE	Q7tsu7 mus musculus	819	127	7.9	1012	2	Q4SW91_TETNG	Q4sw91 tetraodon n
747	129	8.0	723	2	Q5HZP8_XENLA	Q5hzf8 xenopus lae	820	127	7.9	3262	2	Q9EQJ5_MOUSE	Q9eqj5 mus musculus
748	129	8.0	727	2	Q5W5X8_XENLA	Q5w5x8 xenopus lae	821	126.5	7.9	231	2	Q8WY6_HUMAN	Q8wy6 homo sapien
749	129	8.0	769	1	PIGR_RAT	P15083 rattus norv	822	126.5	7.9	306	1	CD80_MOUSE	Q00609 mus musculus
750	129	8.0	782	2	Q4SI43_TETNG	Q4si43 tetraodon n	823	126.5	7.9	306	2	Q549R2_MOUSE	Q549r2 mus musculus
751	129	8.0	867	2	Q5VZW7_HUMAN	Q5vzw7 homo sapien	824	126.5	7.9	353	1	CEPUI_CHICK	Q90773 gallus gall
752	129	8.0	875	2	Q5VZW8_HUMAN	Q5vzw8 homo sapien	825	126.5	7.9	419	1	PSG4_HUMAN	Q00888 homo sapien
753	129	8.0	957	2	Q5TF8_HUMAN	Q5tf88 homo sapien	826	126.5	7.9	419	1	PSG7_HUMAN	Q13046 homo sapien
754	129	8.0	1027	1	CNTN5_CHICK	Q90479 gallus gall	827	126.5	7.9	419	2	Q6P520_HUMAN	Q6p520 homo sapien
755	129	8.0	1028	1	CNTN6_RAT	P97528 rattus norv	828	126.5	7.9	450	2	Q94QL5_HUMAN	Q94ql5 homo sapien
756	129	8.0	1100	2	Q5RKW8_MOUSE	Q5rkw8 mus musculus	829	126.5	7.9	450	2	Q9VR25_DROME	Q9vr25 drosophila
757	129	8.0	1252	2	Q9EQS9_MOUSE	Q9eqs9 mus musculus	830	126.5	7.9	1026	1	CNTN4_MOUSE	Q69226 mus musculus
758	129	8.0	1253	2	Q9EQS8_MOUSE	Q9eqs8 mus musculus	831	126.5	7.9	1083	2	Q76698_CABEL	Q76698 caenorhabdi
759	129	8.0	1269	2	Q6U715_BRARE	Q6u715 brachydanio	832	126.5	7.9	1447	1	DCC_HUMAN	P43146 homo sapien
760	129	8.0	1311	2	Q961K8_DROME	Q961k8 drosophila	833	126.5	7.9	1515	2	Q4SHH6_TETNG	Q4shh6 tetraodon n
761	129	8.0	1527	2	Q9VZZ4_DROME	Q9vzz4 drosophila	834	126.5	7.9	2095	2	Q4RYE5_TETNG	Q4rye5 tetraodon n

835	136	7.9	190	2	Q4SA11_TETNG	Q4sa11 tetraodon n	908	124	7.7	1950	2	Q80YN8_MOUSE	Q80yn8 mus musculus
836	126	7.9	257	2	Q8R202_MOUSE	Q8r202 mus musculus	909	124	7.7	2053	1	DSCL1_HUMAN	Q8t484 homo sapien
837	126	7.9	261	2	Q9D7L8_MOUSE	Q9d7l8 m mus musculus	910	124	7.7	8402	1	Q4RE83_TETNG	Q4re83 tetraodon n
838	126	7.9	465	2	Q59E14_DROME	Q59e14 drosophila	911	123.5	7.7	399	1	CD80_RABIT	P42070 oryctolagus
839	126	7.9	881	2	Q4QR3_TETNG	Q4qr3 tetraodon n	912	123.5	7.7	317	2	Q5TON9_ANOGA	Q5tqn9 anopheles g
840	126	7.9	1028	1	CNTN6_HUMAN	C9nu52 homo sapien	913	123.5	7.7	419	1	PSG1_HUMAN	P11464 homo sapien
841	126	7.9	1028	1	CNTN6_MOUSE	Q9jmb8 mus musculus	914	123.5	7.7	427	2	Q61CR4_HUMAN	Q61cr4 homo sapien
842	126	7.9	1028	2	Q5R6D4_PONPY	Q5r6d4 pongo pygma	915	123.5	7.7	436	2	Q86YV1_HUMAN	Q86yv1 homo sapien
843	126	7.9	1338	1	VGER1_HUMAN	P17948 h vascular	916	123.5	7.7	440	2	Q62MD4_HUMAN	Q62md4 homo sapien
844	126	7.9	1338	2	Q5TARI_HUMAN	Q5tar1 homo sapien	917	123.5	7.7	582	2	Q9SN25_BOVIN	Q9s25 bos taurus
845	126	7.9	1400	2	Q7PF94_ANOGA	Q7pf94 anopheles g	918	123.5	7.7	606	2	Q9SSS7_MOUSE	Q9ses7 mus musculus
846	125.5	7.8	282	2	Q7Z7D3_HUMAN	Q7z7d3 homo sapien	919	123.5	7.7	606	2	Q4T4K0_TETNG	Q4t4k0 tetraodon n
847	125.5	7.8	285	2	Q5T2L0_HUMAN	Q5t2l0 homo sapien	920	123.5	7.7	648	2	Q9EPF1_MOUSE	Q9epf1 mus musculus
848	125.5	7.8	299	2	Q7Q0P9_ANOGA	Q7q0p9 anopheles g	921	123.5	7.7	766	2	Q7Q0S7_ANOGA	Q7q0s7 anopheles g
849	125.5	7.8	306	2	Q9QV14_MOUSE	Q9qv14 mus musculus	922	123.5	7.7	1026	1	CNTN4_RAT	Q62845 rattus norv
850	125.5	7.8	310	2	Q4V8T3_BRARE	Q4v8t3 brachydanio	923	123.5	7.7	1319	2	Q4T8B2_TETNG	Q4t8b2 tetraodon n
851	125.5	7.8	340	2	Q9W3N2_DROME	Q9w3n2 drosophila	924	123.5	7.7	1409	2	Q617L8_CAEBR	Q617l8 caenorhabdi
852	125.5	7.8	341	2	Q61354_MOUSE	Q61354 mus musculus	925	123.5	7.7	3158	2	Q4TAD4_TETNG	Q4tad4 tetraodon n
853	125.5	7.8	352	2	Q08266_HUMAN	Q08266 homo sapien	926	123.5	7.7	26926	2	Q4U1Z6_HUMAN	Q4u1z6 homo sapien
854	125.5	7.8	352	2	Q15403_HUMAN	Q15403 homo sapien	927	123.5	7.7	26926	2	Q8W2B3_HUMAN	Q8w2b3 homo sapien
855	125.5	7.8	465	2	Q640J0_XENLA	Q640j0 xenopus lae	928	123	7.7	302	1	ICOSL1_HUMAN	Q75144 homo sapien
856	125.5	7.8	480	2	Q9PSD1_9PIPI	Q9psd1 xenopus. fi	929	123	7.7	370	2	Q800Y8_BRARE	Q800y8 brachydanio
857	125.5	7.8	510	2	Q801V8_BRARE	Q801v8 brachydanio	930	123	7.7	411	2	Q15228_HUMAN	Q15228 homo sapien
858	125.5	7.8	590	2	Q4SPF8_TETNG	Q4spf8 tetraodon n	931	123	7.7	442	1	SIGL16_HUMAN	Q43699 homo sapien
859	125.5	7.8	769	2	Q8NI15_HUMAN	Q8ni15 homo sapien	932	123	7.7	462	1	Q6GLT3_XENLA	Q6gl13 xenopus lae
860	125.5	7.8	806	1	FGPR3_HUMAN	P22607 homo sapien	933	123	7.7	515	1	PVRI_PIG	Q9176 sus scrofa
861	125.5	7.8	838	2	Q4SPF9_TETNG	Q4spf9 tetraodon n	934	123	7.7	622	2	Q9JKB2_MOUSE	Q9jkb2 mus musculus
862	125.5	7.8	1028	1	CNTN3_HUMAN	Q9p232 homo sapien	935	123	7.7	648	2	Q8R2Y2_MOUSE	Q8r2y2 mus musculus
863	125.5	7.8	1040	2	Q9W675_BRARE	Q9w675 brachydanio	936	123	7.7	656	2	Q4SPF7_TETNG	Q4spf7 tetraodon n
864	125.5	7.8	1154	2	Q4SR22_TETNG	Q4sr22 tetraodon n	937	123	7.7	692	2	Q800Y9_BRARE	Q800y9 brachydanio
865	125.5	7.8	1242	1	NPHN_MOUSE	Q9qze7 mus musculus	938	123	7.7	756	2	Q800Z0_BRARE	Q800z0 brachydanio
866	125.5	7.8	1256	2	Q92555_MOUSE	Q92555 mus musculus	939	123	7.7	776	2	Q4RHT1_TETNG	Q4rht1 tetraodon n
867	125.5	7.8	1256	2	Q9J1X1_MOUSE	Q9j1x1 mus musculus	940	123	7.7	820	2	Q53H63_HUMAN	Q53h63 homo sapien
868	125.5	7.8	1256	2	Q9ET59_MOUSE	Q9et59 mus musculus	941	123	7.7	922	2	Q90413_BRARE	Q90413 brachydanio
869	125.5	7.8	1445	2	Q63155_RAT	Q63155 rattus norv	942	123	7.7	1040	1	CNTN2_HUMAN	Q02246 homo sapien
870	125	7.8	147	1	DCC_MOUSE	Q63155 rattus norv	943	123	7.7	1040	2	Q5T054_HUMAN	Q5t054 homo sapien
871	125	7.8	219	2	Q8W991_HUMAN	Q8w991 mus musculus	944	123	7.7	1091	1	LRIG1_MOUSE	P70193 mus musculus
872	125	7.8	325	2	Q8HW98_MOUSE	Q8hw98 mus musculus	945	123	7.7	1250	2	Q8TDY8_HUMAN	Q8tdy8 homo sapien
873	125	7.8	775	2	Q6PF50_XENLA	Q6pf50 xenopus lae	946	123	7.7	1723	2	Q8CHB2_MOUSE	Q8chb2 mus musculus
874	125	7.8	868	1	MUSK_MOUSE	Q61006 mus musculus	947	123	7.7	4650	2	Q15598_HUMAN	Q15598 homo sapien
875	125	7.8	956	1	NAMC1_HUMAN	Q7z553 homo sapien	948	123	7.7	4824	2	Q15598_HUMAN	Q15598 procambur
876	125	7.8	1100	1	CNTN5_HUMAN	Q94779 homo sapien	949	123	7.7	16215	2	Q9NFS3_DROME	Q9nfs3 drosophila
877	125	7.8	1180	1	Q1S940_PANTR	Q51940 pan troglod	950	123	7.7	18074	2	Q917U4_DROME	Q917u4 drosophila
878	125	7.8	1197	1	L1C41_BRARE	Q90478 brachydanio	951	122.5	7.6	336	2	Q961T8_DROME	Q961t8 drosophila
879	125	7.8	2212	2	Q8NEN3_HUMAN	Q8nhn3 homo sapien	952	122.5	7.6	413	2	Q4H1G8_SAMCR	Q4h1g8 samia cynth
880	125	7.8	18412	2	Q7Z261_BRARE	Q7z261 brachydanio	953	122.5	7.6	633	2	Q5W434_BRARE	Q5w434 brachydanio
881	124.5	7.8	290	2	Q5TNT8_ANOGA	Q5tnt8 anopheles g	954	122.5	7.6	651	2	Q5W433_BRARE	Q5w433 brachydanio
882	124.5	7.8	313	2	Q57596_CHICK	Q57596 gallus gall	955	122.5	7.6	723	2	Q86Y14_HUMAN	Q86y14 homo sapien
883	124.5	7.8	315	2	Q9DG15_CHICK	Q9dg15 gallus gall	956	122.5	7.6	739	2	Q9GKR3_BOVIN	Q9gkr3 bos taurus
884	124.5	7.8	344	2	Q93242_CHICK	Q93242 gallus gall	957	122.5	7.6	821	2	Q4S2G2_TETNG	Q4s2g2 tetraodon n
885	124.5	7.8	419	2	Q68CR6_HUMAN	Q68cr6 homo sapien	958	122.5	7.6	1073	2	Q9TX18_CAEBL	Q9tx18 caenorhabdi
886	124.5	7.8	426	1	PSG8_HUMAN	Q9uq74 homo sapien	959	122.5	7.6	1156	2	Q676C3_9UROC	Q676c3 oikopleura
887	124.5	7.8	822	2	Q9QVV7_9MORI	Q9qv77 rattus sp.	960	122.5	7.6	1746	2	Q8WT19_HUMAN	Q8w19 homo sapien
888	124.5	7.8	1045	2	Q86T37_HUMAN	Q86t37 homo sapien	961	122.5	7.6	2012	1	DSCAM_HUMAN	Q60469 homo sapien
889	124.5	7.8	1045	2	Q5VV36_HUMAN	Q5vv36 homo sapien	962	122.5	7.6	2013	2	Q8VHZ8_RAT	Q8vzh8 rattus norv
890	124.5	7.8	1047	2	Q4RCG7_TETNG	Q4rcg7 tetraodon n	963	122.5	7.6	2023	2	Q59GH3_HUMAN	Q59gh3 homo sapien
891	124.5	7.8	1241	1	NPHN_HUMAN	Q60500 homo sapien	964	122.5	7.6	3100	2	Q7KYN5_HUMAN	Q7kyn5 homo sapien
892	124.5	7.8	1320	2	Q96KF5_HUMAN	Q96kf5 homo sapien	965	122	7.6	312	2	Q4SUX1_TETNG	Q4sux1 tetraodon n
893	124.5	7.8	1320	2	Q86TC9_HUMAN	Q86tc9 homo sapien	966	122	7.6	332	1	CD22_GORGO	Q9nt4 gorilla gor
894	124.5	7.8	1320	2	Q5VV35_HUMAN	Q5vv35 homo sapien	967	122	7.6	513	2	Q9B6N4_MOUSE	Q9b6n4 mus musculus
895	124.5	7.8	1391	2	Q8N3L4_HUMAN	Q8n3l4 homo sapien	968	122	7.6	582	2	Q8R4B5_MOUSE	Q8r4b5 mus musculus
896	124.5	7.8	5724	2	Q7PT04_ANOGA	Q7pt04 anopheles g	969	122	7.6	595	2	Q7Q3K8_ANOGA	Q7q3k8 anopheles g
897	124.5	7.8	8625	2	Q86GD6_PROCL	Q86gd6 procambur	970	122	7.6	813	1	FGPR2_XENLA	Q03364 xenopus lae
898	124	7.7	253	2	Q9D8H2_MOUSE	Q9d8h2 m mus muscu	971	122	7.6	907	2	Q9NEG0_DROME	Q9neg0 drosophila
899	124	7.7	585	1	CEA20_HUMAN	Q6uy09 homo sapien	972	122	7.6	915	2	Q8R4B3_MOUSE	Q8r4b3 mus musculus
900	124	7.7	879	2	Q59FL9_HUMAN	Q59fl9 homo sapien	973	122	7.6	1066	2	Q8MSR5_DROME	Q8msr5 drosophila
901	124	7.7	997	2	Q44087_CAEBL	Q44087 caenorhabdi	974	122	7.6	1166	2	Q9QVN4_9MURI	Q9qvn4 rattus sp.
902	124	7.7	1028	1	CNTN3_RAT	Q62682 rattus norv	975	122	7.6	1232	2	Q8TCG8_HUMAN	Q8tcg8 homo sapien
903	124	7.7	1034	1	LRIG2_MOUSE	Q52kr2 mus musculus	976	122	7.6	1252	2	Q9J1X2_RAT	Q9j1x2 rattus norv
904	124	7.7	1284	1	NRCAM_CHICK	P35331 gallus gall	977	122	7.6	1388	2	Q624K5_CAEBR	Q624k5 caenorhabdi
905	124	7.7	1443	2	Q8MTB2_DROME	Q8mtb2 drosophila	978	122	7.6	1302	1	VGRF2_BRARE	Q8axb3 brachydanio
906	124	7.7	1765	2	Q9VS30_DROME	Q9vs30 drosophila	979	122	7.6	3215	2	Q8IRV7_DROME	Q8irv7 drosophila
907	124	7.7	1770	2	Q9VS29_DROME	Q9vs29 drosophila	980	122	7.6	4117	2	Q8IRV9_DROME	Q8irv9 drosophila

981	122	7.6	4179	2	Q9MAY4_DROME	Q9w4y4_drosophila	1054	120	7.5	459	2	Q86X91_HUMAN	Q86x91_homo sapien
982	122	7.6	4223	2	Q8MEN3_DROME	Q8mpn3_drosophila	1055	120	7.5	483	2	Q7SX76_BARE	Q7sx76_brachydanio
983	122	7.6	4228	2	Q8IRV8_DROME	Q8irv8_drosophila	1056	120	7.5	524	1	BT1A1_MOUSE	Q5246_mus musculus
984	122	7.6	5516	2	Q7Z248_BARE	Q7z248_brachydanio	1057	120	7.5	524	2	Q5SQU6_MOUSE	Q5squ6_mus musculus
985	121.5	7.6	304	2	Q9TXQ1_CANFA	Q9txq1_canis famil	1058	120	7.5	677	2	Q8QHL2_CHICK	Q8qhl2_gallus gall
986	121.5	7.6	332	1	PSG11_HUMAN	Q9uqx1_homo sapien	1059	120	7.5	773	2	Q59FV9_HUMAN	Q59fv9_homo sapien
987	121.5	7.6	338	2	Q723W6_HUMAN	Q723w6_homo sapien	1060	120	7.5	814	2	Q59H40_HUMAN	Q59h40_homo sapien
988	121.5	7.6	338	2	Q5RTT4_PONPY	Q5rtt4_pongo pygma	1061	120	7.5	820	2	Q5R8Q3_PONPY	Q5r8q3_pongo pygma
989	121.5	7.6	434	1	PSG10_HUMAN	Q15235_homo sapien	1062	120	7.5	822	1	FGFR1_HUMAN	F11362_homo sapien
990	121.5	7.6	428	1	PSG3_HUMAN	Q16557_homo sapien	1063	120	7.5	822	1	FGFR1_MOUSE	P16092_mus musculus
991	121.5	7.6	428	2	Q9BRW2_HUMAN	Q9brw2_homo sapien	1064	120	7.5	822	1	FGFR1_RAT	Q04589_rattus norv
992	121.5	7.6	435	1	PSG6_HUMAN	Q00889_homo sapien	1065	120	7.5	822	2	Q60818_MOUSE	Q60818_mus musculus
993	121.5	7.6	602	2	Q52NV2_RAT	Q52nv2_rattus norv	1066	120	7.5	888	2	Q4VBK2_BARE	Q4vbk2_brachydanio
994	121.5	7.6	775	2	Q97754_RABIT	Q97754_oryctolagus	1067	120	7.5	939	2	Q4VBK2_BARE	Q4vbk2_brachydanio
995	121.5	7.6	898	1	FAS2_SCHAM	P22648_schistocerc	1068	120	7.5	1014	2	Q8NFA6_HUMAN	Q8nfa6_homo sapien
996	121.5	7.6	987	2	Q7YZM8_CAEEL	Q7yzm8_caenorhabdi	1069	120	7.5	1168	2	Q5U3B1_BARE	Q5u3b1_brachydanio
997	121.5	7.6	1379	2	Q5XNV9_PETMA	Q5xnv9_petromyzon	1070	120	7.5	1205	2	Q8BUJ0_MOUSE	Q8bujo_mus musculus
998	121.5	7.6	1415	2	Q5XNV8_PETMA	Q5xnv8_petromyzon	1071	120	7.5	1327	2	Q8QHL3_CHICK	Q8qhl3_gallus gall
999	121.5	7.6	2013	2	Q9ERC8_MOUSE	Q9erc8_mus musculus	1072	120	7.5	1332	2	Q9BN17_DROME	Q9bn17_drosophila
1000	121.5	7.6	4816	2	Q8T103_BOMMO	Q8t103_bombyx mori	1073	120	7.5	1332	2	Q9QVW7_DROME	Q9qv7_drosophila
1001	121	7.5	182	2	Q15402_HUMAN	Q15402_homo sapien	1074	120	7.5	1725	2	Q7Q9I6_ANOGA	Q7q9i6_anopheles g
1002	121	7.5	294	2	Q8BH36_MESAU	Q8bh36_mesocricetu	1075	120	7.5	9369	2	Q4T444_TETNG	Q4t444_tetraodon n
1003	121	7.5	316	2	Q8HUN1_HUMAN	Q8hun1_homo sapien	1076	119.5	7.4	200	2	Q7PYG0_ANOGA	Q7pygo_anopheles g
1004	121	7.5	318	2	Q90293_BRARE	Q90293_brachydanio	1077	119.5	7.4	282	2	Q9H6B2_HUMAN	Q9h6b2_homo sapien
1005	121	7.5	319	2	Q8MT24_DROME	Q8mt24_drosophila	1078	119.5	7.4	287	2	Q13984_HUMAN	Q13984_homo sapien
1006	121	7.5	328	2	Q8UV66_BARE	Q8uv66_brachydanio	1079	119.5	7.4	345	1	OPCM_RAT	P32736_rattus norv
1007	121	7.5	337	2	Q6DFY2_MOUSE	Q6dfy2_mus musculus	1080	119.5	7.4	386	2	Q4S1B2_TETNG	Q4s1b2_tetraodon n
1008	121	7.5	360	2	Q61565_MOUSE	Q61565_mus musculus	1081	119.5	7.4	509	1	SHPS1_RAT	P97710_r tyrosine-
1009	121	7.5	361	2	Q9QW79_9MURI	Q9qw79_mus sp. fib	1082	119.5	7.4	543	2	Q62218_CABER	Q62218_caenorhabdi
1010	121	7.5	422	2	Q96PJ3_HUMAN	Q96pj3_homo sapien	1083	119.5	7.4	622	2	Q9ESS5_MOUSE	Q9es5_mus musculus
1011	121	7.5	515	2	Q96RE0_HUMAN	Q96re0_homo sapien	1084	119.5	7.4	622	2	Q9R069_MOUSE	Q9r069_mus musculus
1012	121	7.5	515	2	Q96FJ5_HUMAN	Q96fj5_homo sapien	1085	119.5	7.4	736	2	Q8MYS2_DROME	Q8mys2_drosophila
1013	121	7.5	557	2	Q4RB52_TETNG	Q4rb52_tetraodon n	1086	119.5	7.4	739	1	VCAM1_CANFA	Q28260_canis famil
1014	121	7.5	640	2	Q8BSM2_MOUSE	Q8bsm2_mus musculus	1087	119.5	7.4	771	2	Q4RMQ7_HUMAN	Q4rmq7_homo sapien
1015	121	7.5	715	2	Q8S083_DROME	Q8s083_drosophila	1088	119.5	7.4	774	2	Q9V930_DROME	Q9v930_drosophila
1016	121	7.5	733	2	Q8S083_TRIVU	Q8s083_trichoaurus	1089	119.5	7.4	907	2	Q98850_CARAU	Q98850_carassius a
1017	121	7.5	820	2	Q8CTM9_MOUSE	Q8ctm9_mus musculus	1090	119.5	7.4	1134	2	Q71B05_BARE	Q71b05_brachydanio
1018	121	7.5	867	2	Q59DZ1_DROME	Q59dz1_drosophila	1091	119.5	7.4	1304	1	NRCAM_HUMAN	Q92823_homo sapien
1019	121	7.5	1018	1	CNTN1_BOVIN	Q28106_bos taurus	1092	119.5	7.4	1377	1	NEO1_RAT	P97603_rattus norv
1020	121	7.5	1040	2	Q5RDT8_PONPY	Q5rdt8_pongo pygma	1093	119	7.4	177	2	Q6NDR8_HUMAN	Q6nur8_homo sapien
1021	121	7.5	1124	2	Q6P6L5_MOUSE	Q6p6l5_mus musculus	1094	119	7.4	229	2	Q7PUC4_ANOGA	Q7puc4_anopheles g
1022	121	7.5	1171	2	Q86TA8_HUMAN	Q86ta8_homo sapien	1095	119	7.4	291	2	Q53X85_HUMAN	Q53x85_homo sapien
1023	121	7.5	1234	1	NPHN_RAT	Q9r044_rattus norv	1096	119	7.4	306	2	Q5H2T7_XENTR	Q5ht27_xenopus tro
1024	120.5	7.5	1398	2	Q6NVX7_HUMAN	Q6nvx7_homo sapien	1097	119	7.4	310	1	FCG2B_HUMAN	P31994_homo sapien
1025	120.5	7.5	280	2	Q73716_GRUAM	Q73716_grus americ	1098	119	7.4	310	2	Q5VXA9_HUMAN	Q5vxa9_homo sapien
1026	120.5	7.5	285	2	Q7Y330_XENLA	Q7y330_xenopus lae	1099	119	7.4	323	1	FCG2C_HUMAN	P31995_homo sapien
1027	120.5	7.5	327	1	MOX2R_RAT	Q9es58_rattus norv	1100	119	7.4	342	2	Q5JXA9_HUMAN	Q5jxa9_homo sapien
1028	120.5	7.5	341	2	Q8JTX8_LSDV	Q8jtx8_lumpy akin	1101	119	7.4	454	1	BTNL2_RAT	Q6mg97_rattus norv
1029	120.5	7.5	362	2	Q9JH01_RAT	Q9jhg1_rattus norv	1102	119	7.4	481	2	Q6OND3_CABER	Q6ond3_caenorhabdi
1030	120.5	7.5	446	2	Q63236_RAT	Q63236_rattus norv	1103	119	7.4	515	1	PVR1_MOUSE	Q9jfk6_mus musculus
1031	120.5	7.5	446	2	Q63237_RAT	Q63237_rattus norv	1104	119	7.4	515	2	Q6P9M9_MOUSE	Q6p9m9_mus musculus
1032	120.5	7.5	466	2	Q4VMT2_9PIPI	Q4vmt2_xenopus sp.	1105	119	7.4	627	2	Q5RDU0_PONPY	Q5rduo_pongo pygma
1033	120.5	7.5	678	2	Q5XU11_SHEEP	Q5xu11_ovis aries	1106	119	7.4	765	2	Q9TWA4_APLCA	Q9twa4_aplysia cal
1034	120.5	7.5	808	1	FGPR4_MOUSE	Q03142_mus musculus	1107	119	7.4	765	2	Q9BK01_APLCA	Q9bk01_aplysia cal
1035	120.5	7.5	810	2	Q7PUH1_ANOGA	Q7puh1_anopheles g	1108	119	7.4	812	2	Q9BKQ0_APLCA	Q9bkq0_aplysia cal
1036	120.5	7.5	821	1	FGFR2_HUMAN	F21802_homo sapien	1109	119	7.4	812	2	Q9TWA5_APLCA	Q9twa5_aplysia cal
1037	120.5	7.5	1026	1	CNTN4_HUMAN	F21802_homo sapien	1110	119	7.4	816	2	Q91285_PLEWA	Q91285_pleurodeles
1038	120.5	7.5	1049	2	Q4SOF2_TETNG	Q4s0f2_tetraodon n	1111	119	7.4	862	2	Q4SST3_TETNG	Q4sst3_tetraodon n
1039	120.5	7.5	1276	2	Q90X22_BRARE	Q90x22_brachydanio	1112	119	7.4	865	2	Q68DA2_HUMAN	Q68da2_homo sapien
1040	120.5	7.5	1944	2	Q4SPG3_TETNG	Q4spg3_tetraodon n	1113	119	7.4	932	2	Q9TWA6_APLCA	Q9twa6_aplysia cal
1041	120.5	7.5	2222	2	Q97394_DROME	Q97394_drosophila	1114	119	7.4	932	2	Q9BKP9_APLCA	Q9bkp9_aplysia cal
1042	120.5	7.5	4203	2	Q965G2_CABEL	Q965g2_caenorhabdi	1115	119	7.4	961	1	ROBO4_RAT	Q80w87_rattus norv
1043	120.5	7.5	4219	2	Q9NL87_CABEL	Q9nl87_caenorhabdi	1116	119	7.4	1007	1	ROBO4_HUMAN	Q8w275_homo sapien
1044	120.5	7.5	4250	2	Q5PY59_CABEL	Q5py59_caenorhabdi	1117	119	7.4	1018	1	CNTN1_HUMAN	Q12860_homo sapien
1045	120.5	7.5	4369	2	Q8MXD7_CABEL	Q8mxd7_caenorhabdi	1118	119	7.4	8930	2	Q7KQP7_DROME	Q7kqp7_drosophila
1046	120.5	7.5	4889	2	Q9TXK2_CABEL	Q9txk2_caenorhabdi	1119	119	7.4	19066	2	Q801W8_BRARE	Q801w8_brachydanio
1047	120	7.5	200	2	Q4RRS2_TETNG	Q4rrs2_tetraodon n	1120	118.5	7.4	230	2	Q9N164_PAPHA	Q9n164_papio hamad
1048	120	7.5	238	2	Q20339_CABEL	Q20339_caenorhabdi	1121	118.5	7.4	294	2	Q8SPW3_MACPA	Q8spw3_macaca fasc
1049	120	7.5	298	2	Q8INK5_DROME	Q8ink5_drosophila	1122	118.5	7.4	308	2	Q9UFM8_HUMAN	Q9ufm8_homo sapien
1050	120	7.5	357	2	Q18872_PIG	Q18872_sus scrofa	1123	118.5	7.4	317	1	FCG2A_HUMAN	P12318_homo sapien
1051	120	7.5	366	2	Q9N680_DROME	Q9n680_drosophila	1124	118.5	7.4	319	2	Q5ISM6_MACFA	Q5ism6_macaca fasc
1052	120	7.5	376	2	Q9QW78_9MURI	Q9qw78_mus sp. fib	1125	118.5	7.4	410	2	Q4FAT1_BOMMO	Q4fat1_bombyx mori
1053	120	7.5	399	1	VSIG4_HUMAN	Q9y279_homo sapien	1126	118.5	7.4	432	2	Q52NV1_RAT	Q52nv1_rattus norv

1127 118.5 7.4 477 2 Q5EJA2_FUGRU
1128 118.5 7.4 478 2 Q4RVMO_TETNG
1129 118.5 7.4 534 2 Q25403_LYMST
1130 118.5 7.4 646 1 MUC18_HUMAN
1131 118.5 7.4 650 2 Q99K86_MOUSE
1132 118.5 7.4 739 1 VCAM1_HUMAN
1133 118.5 7.4 739 2 Q53FL7_HUMAN
1134 118.5 7.4 829 2 Q4RIG0_TETNG
1135 118.5 7.4 877 2 Q9GSH3_HALFO
1136 118.5 7.4 1065 2 Q4RH24_TETNG
1137 118.5 7.4 1098 2 Q5RGJ3_BRARE
1138 118.5 7.4 1115 2 Q5RGF5_BRARE
1139 118.5 7.4 1119 1 LRIG3_HUMAN
1140 118.5 7.4 1280 2 Q9BFX2_MOUSE
1141 118.5 7.4 1443 1 NEOL1_CHICK
1142 118.5 7.4 1694 1 SN_MOUSE
1143 118.5 7.4 2007 2 Q5W888_TETNG
1144 118.5 7.4 6658 2 Q76281_DROME
1145 118 7.4 218 2 Q6ZMC6_HUMAN
1146 118 7.4 282 2 Q501W4_RAT
1147 118 7.4 289 2 Q5JXB0_HUMAN
1148 118 7.4 316 2 Q8W64_HUMAN
1149 118 7.4 317 2 Q86915_9POXV
1150 118 7.4 326 2 Q9UPK8_HUMAN
1151 118 7.4 328 2 Q8JU20_LSDV
1152 118 7.4 337 2 Q5D095_MOUSE
1153 118 7.4 341 2 Q91WZ1_LSDV
1154 118 7.4 422 2 Q8W61_LYMDI
1155 118 7.4 429 2 Q60F95_HUMAN
1156 118 7.4 567 1 ILRL1_MOUSE
1157 118 7.4 584 2 Q9Y3Y8_HUMAN
1158 118 7.4 602 2 Q9VFD9_DROME
1159 118 7.4 941 2 Q5J1R9_BRARE
1160 118 7.4 949 1 MAMC1_MOUSE
1161 118 7.4 1032 1 CNTN2_BRARE
1162 118 7.4 1148 2 Q86T39_HUMAN
1163 118 7.4 1154 2 Q9QVN3_9MURI
1164 118 7.4 1194 2 Q6PW35_RAT
1165 118 7.4 1197 2 Q6PW38_RAT
1166 118 7.4 1198 2 Q6PW37_RAT
1167 118 7.4 1206 2 Q6PW36_RAT
1168 118 7.4 1209 2 Q6PW39_RAT
1169 118 7.4 1214 1 NRCAM_RAT
1170 118 7.4 1256 1 NRCAM_MOUSE
1171 118 7.4 1299 2 Q6PW34_RAT
1172 118 7.4 6875 2 Q28733_RABIT
1173 118 7.4 8647 2 Q7KQP5_DROME
1174 118 7.4 8648 2 Q7KQP6_DROME
1175 118 7.4 8943 2 Q9VA47_DROME
1176 117.5 7.3 173 2 Q7PSS8_ANOGA
1177 117.5 7.3 265 2 Q61XU3_CAEBR
1178 117.5 7.3 278 2 Q99232_MOUSE
1179 117.5 7.3 323 2 Q563Y2_ONCMY
1180 117.5 7.3 332 2 Q8TA95_HUMAN
1181 117.5 7.3 336 2 Q5ISAG_9PRIM
1182 117.5 7.3 391 2 Q76CT6_MOUSE
1183 117.5 7.3 400 2 Q4T054_TETNG
1184 117.5 7.3 441 2 Q8CI39_MOUSE
1185 117.5 7.3 495 2 Q4TAJ7_TETNG
1186 117.5 7.3 782 2 Q9TTZ3_RABIT
1187 117.5 7.3 800 2 Q918X3_BRARE
1188 117.5 7.3 819 1 FGFR1_CHICK
1189 117.5 7.3 879 2 Q8V199_RAT
1190 117.5 7.3 888 2 Q8VIA0_RAT
1191 117.5 7.3 939 2 Q967X6_DROME
1192 117.5 7.3 939 2 Q9VB35_DROME
1193 117.5 7.3 1005 2 P79921_XENLA
1194 117.5 7.3 1238 2 Q4SS56_TETNG
1195 117 7.3 279 2 Q563G9_ONCMY
1196 117 7.3 293 2 Q563H1_ONCMY
1197 117 7.3 316 1 FCG2A_PANTR
1198 117 7.3 330 1 CD22_PONPY
1199 117 7.3 351 2 Q8JFU3_BRARE

Q5eaj2 fugu rubrip
Q4rvmo tetraodon n
Q25403 lymaea sta
P43121 homo sapien
Q99k86 mus musculu
P19320 homo sapien
Q53fi7 homo sapien
Q4rigo tetraodon n
Q9gsh3 halocynthia
Q4rh24 tetraodon n
Q5rgj3 brachydanio
Q5rgf5 brachydanio
Q6uxm1 homo sapien
Q9epx2 mus musculu
Q90610 gallus gall
Q62230 mus musculu
Q4sm88 tetraodon n
Q76281 drosophila
Q6zmc6 homo sapien
Q501w4 rattus norv
Q5jxb0 homo sapien
Q8w64 homo sapien
Q86915 sheeppox vi
Q9upk8 homo sapien
Q8ju20 lumpy skin
Q5d095 mus musculu
Q91wz1 lumpy skin
Q8w61 lymantria d
Q60f95 homo sapien
P14719 mus musculu
Q9y3y8 homo sapien
Q9vfd9 drosophila
Q5j1r9 brachydanio
P60755 mus musculu
Q8ax24 brachydanio
Q86t39 rattus norv
Q9qvn3 rattus sp.
Q6pw35 rattus norv
Q6pw38 rattus norv
Q6pw37 rattus norv
Q6pw36 rattus norv
Q6pw39 rattus norv
P97686 rattus norv
Q810u4 mus musculu
Q6pw34 rattus norv
Q28733 cryotolagus
Q7kqp5 drosophila
Q7kqp6 drosophila
Q9v4f7 drosophila
Q7pss8 anopheles g
Q61xu3 caenorhabdi
Q99232 mus musculu
Q563y2 oncorhynch
Q8ta95 homo sapien
Q5isa8 saimiri bol
Q76ct6 mus musculu
Q4t054 tetraodon n
Q8ci39 mus musculu
Q4taj7 tetraodon n
Q9ttz3 cryotolagus
Q918x3 brachydanio
P21804 gallus gall
Q8vi99 rattus norv
Q8via0 rattus norv
Q967x6 drosophila
Q9vb35 drosophila
P79921 xenopus lae
Q4ss56 tetraodon n
Q563g9 oncmym
Q563h1 oncmym
Q8spv8 pan troglod
Q9n1e3 pongo pygma
Q8jfu3 brachydanio

Q7ey58 brachydanio
Q5r645 pongo pygma
Q99jq8 mus musculu
Q6q147 bos taurus
P97797 m tyrosine-
Q9qyq7 mus musculu
Q6mg92 rattus norv
Q6b515 poephila gu
Q7pqm9 anopheles g
Q81z77 homo sapien
P60756 rattus norv
Q8uvr9 fugu rubrip
Q596x0 carassius a
Q4sbz7 tetraodon n
P22063 rattus norv
Q9vqm1 drosophila
Q9hcl6 homo sapien
Q7qhc6 anopheles g
Q563h0 oncorhynch
Q75238 homo sapien
Q9ia24 sphaeroides
P11834 bos taurus
Q14982 homo sapien
Q51861 pan troglod
Q80v04 mus musculu
Q15227 homo sapien
Q96360 hypanthia
Q00887 homo sapien
Q6leu7 homo sapien
Q00481 homo sapien
Q8bj62 mus musculu
Q95xj7 caenorhabdi
Q6phr3 homo sapien
Q95812 homo sapien
Q59e86 homo sapien
Q61v11 caenorhabdi
P29534 rattus norv
Q5fv83 rattus norv
P01833 homo sapien
Q68d81 homo sapien
Q95r27 drosophila
Q9w4y6 drosophila
Q9y619 homo sapien
Q569k7 homo sapien
Q00872 homo sapien
Q8n312 homo sapien
Q8n3r4 homo sapien
Q86tc8 homo sapien
Q86t48 homo sapien
Q03696 gallus gall
Q4rw80 tetraodon n
Q7q0x2 anopheles g
Q5tnw7 anopheles g
Q8wz51 homo sapien
Q61853 caenorhabdi
Q7rt14 drosophila
Q15108 homo sapien
Q4scu0 tetraodon n
Q8spw4 macaca fasc
Q6uxg3 homo sapien
Q15238 homo sapien
Q6gm08 xenopus lae
Q960d1 drosophila
Q5w431 fugu rubrip
Q5w436 fugu rubrip
Q5w435 fugu rubrip
Q5bj23 mus musculu
Q8n116 homo sapien
Q4st7 tetraodon n
Q7q086 anopheles g
Q8c310 mus musculu
Q9vzt8 drosophila

1273	116	7.2	1461	2	Q8T9P6_DROME	Q8t9f6 drosophila
1274	116	7.2	1509	2	Q9VLQ8_DROME	Q9v1q8 drosophila
1275	116	7.2	1933	2	Q6V3A4_MOUSE	Q6v3a4 mus musculus
1276	116	7.2	2159	2	Q6PAL2_MOUSE	Q6pal2 mus musculus
1277	116	7.2	2558	2	Q6NR91_DROME	Q6nr91 drosophila
1278	116	7.2	2828	2	Q9NR99_HUMAN	Q9nr99 homo sapien
1279	115.5	7.2	180	2	Q15107_HUMAN	Q15107 homo sapien
1280	115.5	7.2	187	2	Q6P097_HUMAN	Q6p097 homo sapien
1281	115.5	7.2	189	2	Q15106_HUMAN	Q15106 homo sapien
1282	115.5	7.2	288	2	Q28499_MACMU	Q28499 macaca mulla
1283	115.5	7.2	296	2	Q8WMZ2_PIG	Q8wmz2 sus scrofa
1284	115.5	7.2	324	2	Q9UPK9_HUMAN	Q9upk9 homo sapien
1285	115.5	7.2	332	2	Q5SPT4_BRARE	Q5spt4 brachydanio
1286	115.5	7.2	335	2	Q75237_HUMAN	Q75237 homo sapien
1287	115.5	7.2	398	2	Q5SX11_HUMAN	Q5sx11 homo sapien
1288	115.5	7.2	410	2	Q6R3L9_BOMMA	Q6r3l9 bombyx mand
1289	115.5	7.2	410	2	Q6R3M0_BOMMO	Q6r3m0 bombyx mori
1290	115.5	7.2	410	2	Q6R3M2_BOMMO	Q6r3m2 bombyx mori
1291	115.5	7.2	422	2	Q86CY9_HELAM	Q86cy9 helicoverpa
1292	115.5	7.2	452	2	Q4R5Y9_MACFA	Q4r5y9 macaca fasc
1293	115.5	7.2	513	2	Q53F15_HUMAN	Q53f15 homo sapien
1294	115.5	7.2	517	1	PVR1_HUMAN	Q15223 homo sapien
1295	115.5	7.2	626	2	Q4SMG6_TETNG	Q4smg6 tetraodon n
1296	115.5	7.2	636	2	Q22040_CABEL	Q22040 caenorhabdi
1297	115.5	7.2	731	2	Q8SP16_MACEU	Q8sp16 macropus eu
1298	115.5	7.2	743	2	Q8R6B2_5CAUD	Q8r6b2 vibrio phag
1299	115.5	7.2	755	2	Q8CCF8_MOUSE	Q8ccf8 mus musculus
1300	115.5	7.2	824	2	Q91286_PLEWA	Q91286 pleurodeles
1301	115.5	7.2	879	2	Q6PE80_MOUSE	Q6pe80 mus musculus
1302	115.5	7.2	888	1	UFO_MOUSE	Q00993 mus musculus
1303	115.5	7.2	888	2	Q807Q3_MOUSE	Q807q3 mus musculus
1304	115.5	7.2	1248	2	Q9XR41_CERAB	Q9xr41 cercopithec
1305	115.5	7.2	2325	2	Q9NX38_CABEL	Q9nx38 caenorhabdi
1306	115.5	7.2	3317	2	Q7QJK9_ANOGA	Q7qjk9 anopheles g
1307	115	7.2	151	2	Q6JDC3_DISGA	Q6jdc3 disostichu
1308	115	7.2	226	2	Q8N440_HUMAN	Q8n440 homo sapien
1309	115	7.2	262	2	Q80770_MOUSE	Q80770 mus musculus
1310	115	7.2	287	2	Q4SL89_TETNG	Q4sl89 tetraodon n
1311	115	7.2	308	2	Q7Q863_ANOGA	Q7q863 anopheles g
1312	115	7.2	326	2	Q8NC17_HUMAN	Q8nc17 homo sapien
1313	115	7.2	344	2	Q6B014_HUMAN	Q6b014 homo sapien
1314	115	7.2	346	2	Q9CTL3_MOUSE	Q9ctl3 mus musculus
1315	115	7.2	348	1	NEGR1_MOUSE	Q80224 mus musculus
1316	115	7.2	351	2	Q15225_HUMAN	Q15225 homo sapien
1317	115	7.2	352	1	NEGR1_HUMAN	Q723b1 homo sapien
1318	115	7.2	354	2	Q5VT21_HUMAN	Q5vt21 homo sapien
1319	115	7.2	364	2	Q6GNC2_XENLA	Q6gnc2 xenopus lae
1320	115	7.2	509	2	Q6PE18_MOUSE	Q6pe18 mus musculus
1321	115	7.2	548	2	Q7PMJ7_ANOGA	Q7pmj7 anopheles g
1322	115	7.2	600	2	Q8N7W7_HUMAN	Q8n7w7 homo sapien
1323	115	7.2	602	1	NRG1_CHICK	Q05199 gallus gall
1324	115	7.2	649	2	Q59F24_HUMAN	Q59f24 homo sapien
1325	115	7.2	823	1	CEK3_CHICK	P18461 gallus gall
1326	115	7.2	824	2	Q90749_CHICK	Q90749 gallus gall
1327	115	7.2	912	1	ICAM5_EBIBT	Q28730 cryptotagus
1328	115	7.2	917	1	ICAM5_MOUSE	Q60625 mus musculus
1329	115	7.2	1040	1	CNTN2_MOUSE	Q61330 mus musculus
1330	115	7.2	1255	2	Q723Z9_HUMAN	Q723z9 homo sapien
1331	115	7.2	1255	2	Q7YQL8_PANTR	Q7yql8 pan troglod
1332	115	7.2	1257	1	L1CAM_HUMAN	P32004 homo sapien
1333	115	7.2	1298	1	VGRF3_HUMAN	P35916 homo sapien
1334	115	7.2	2242	2	Q9P2P9_HUMAN	Q9p2p9 homo sapien
1335	115	7.2	2322	2	Q60ZN5_CABER	Q60zn5 caenorhabdi
1336	115	7.2	3094	2	Q695L1_HUMAN	Q695l1 homo sapien
1337	114.5	7.1	321	2	O55202_RAT	O55202 rattus norv
1338	114.5	7.1	341	2	Q61353_MOUSE	Q61353 mus musculus
1339	114.5	7.1	361	2	Q8R4B1_MOUSE	Q8r4b1 mus musculus
1340	114.5	7.1	413	2	Q26438_HYACE	Q26438 hyalophora
1341	114.5	7.1	510	2	Q96K15_HUMAN	Q96k15 homo sapien
1342	114.5	7.1	510	2	Q96NY8_HUMAN	Q96ny8 homo sapien
1343	114.5	7.1	534	2	Q866T2_PANTR	Q866t2 pan troglod
1344	114.5	7.1	540	2	Q4RRT9_TETNG	Q4rrt9 tetraodon n
1345	114.5	7.1	562	2	Q6TNR7_BRARE	Q6tnr7 brachydanio

1346	114.5	7.1	699	2	Q622N7_CABER	Q622n7 caenorhabdi
1347	114.5	7.1	739	2	Q5R847_PONPY	Q5r847 pongo pygma
1348	114.5	7.1	740	1	PECAL_PIG	Q9S242 sus scrofa
1349	114.5	7.1	821	1	GFPR2_MOUSE	P21803 mus musculus
1350	114.5	7.1	875	2	Q91ZY7_MOUSE	Q91zy7 mus musculus
1351	114.5	7.1	878	2	Q9GV22_MYGA	Q9gv22 mytilus gal
1352	114.5	7.1	1009	2	Q93250_XENLA	Q93250 xenopus lae
1353	114.5	7.1	1255	2	Q7YQL7_PONPY	Q7yql7 pongo pygma
1354	114.5	7.1	1389	2	Q4VA61_MOUSE	Q4va61 mus musculus
1355	114	7.1	145	2	Q9MZE4_MACMU	Q9mze4 macaca mulla
1356	114	7.1	182	2	Q15232_HUMAN	Q15232 homo sapien
1357	114	7.1	189	2	Q15230_HUMAN	Q15230 homo sapien
1358	114	7.1	206	2	Q03679_MOUSE	Q03679 mus musculus
1359	114	7.1	242	2	Q9N165_PAPHA	Q9n165 papio hamad
1360	114	7.1	283	2	Q9VT76_DROME	Q9vt76 drosophila
1361	114	7.1	344	2	Q8WR42_CABEL	Q8wr42 caenorhabdi
1362	114	7.1	345	2	Q8MPV0_CABEL	Q8mpv0 caenorhabdi
1363	114	7.1	348	1	NEGR1_RAT	Q9z0j8 rattus norv
1364	114	7.1	430	2	Q7QCP2_ANOGA	Q7qcp2 anopheles g
1365	114	7.1	435	2	Q8WR44_CABEL	Q8wr44 caenorhabdi
1366	114	7.1	436	2	Q8MPV1_CABEL	Q8mpv1 caenorhabdi
1367	114	7.1	443	2	Q8WR43_CABEL	Q8wr43 caenorhabdi
1368	114	7.1	444	2	Q8MPU9_CABEL	Q8mpu9 caenorhabdi
1369	114	7.1	506	2	Q6MG91_RAT	Q6mg91 rattus norv
1370	114	7.1	570	2	Q6GMZ9_XENLA	Q6gmz9 xenopus lae
1371	114	7.1	588	2	Q4RFF0_TETNG	Q4rff0 tetraodon n
1372	114	7.1	875	2	Q4RKK6_TETNG	Q4rkk6 tetraodon n
1373	114	7.1	1240	1	NFASC_MOUSE	Q810u3 mus musculus
1374	114	7.1	1251	2	Q6ZQ54_MOUSE	Q6zq54 mus musculus
1375	114	7.1	1260	1	L1CAM_MOUSE	P11627 mus musculus
1376	114	7.1	1274	1	MYPC3_HUMAN	Q14896 homo sapien
1377	114	7.1	1274	2	Q9UMS3_HUMAN	Q9ums3 homo sapien
1378	114	7.1	1415	2	Q94155_CABEL	Q94155 caenorhabdi
1379	113.5	7.1	288	2	Q77684_MACNE	Q77684 macaca neme
1380	113.5	7.1	324	2	Q8NBY8_HUMAN	Q8nby8 homo sapien
1381	113.5	7.1	328	2	Q5SYE1_BRARE	Q5syel1 brachydanio
1382	113.5	7.1	413	1	HENO_HYACE	P25033 hyalophora
1383	113.5	7.1	417	1	PVR_HUMAN	P15151 homo sapien
1384	113.5	7.1	422	2	Q502A9_BRARE	Q502a9 brachydanio
1385	113.5	7.1	455	2	Q4RDF3_TETNG	Q4rdf3 tetraodon n
1386	113.5	7.1	527	2	Q4SZU1_TETNG	Q4szu1 tetraodon n
1387	113.5	7.1	620	1	SWP_COIJA	Q92154 coturnix co
1388	113.5	7.1	628	1	LU_HUMAN	P50895 homo sapien
1389	113.5	7.1	637	2	Q7RTW3_HUMAN	Q7rtw3 homo sapien
1390	113.5	7.1	681	2	Q5DUF3_CHICK	Q5duf3 gallus gall
1391	113.5	7.1	695	1	IRPL1_MOUSE	P59823 mus musculus
1392	113.5	7.1	696	1	IRPL1_RAT	P59824 rattus norv
1393	113.5	7.1	703	2	Q21135_CABEL	Q21139 caenorhabdi
1394	113.5	7.1	729	2	Q91147_NOTVI	Q91147 notophthalm
1395	113.5	7.1	753	2	Q5J7D9_MOUSE	Q5j7d9 mus musculus
1396	113.5	7.1	799	2	Q8C3V5_MOUSE	Q8c3v5 mus musculus
1397	113.5	7.1	799	2	Q8CIB8_MOUSE	Q8cib8 mus musculus
1398	113.5	7.1	806	1	CEK2_CHICK	P18460 gallus gall
1399	113.5	7.1	989	2	Q4STG8_TETNG	Q4stg8 tetraodon n
1400	113.5	7.1	1021	1	CNTN1_RAT	Q63198 rattus norv
1401	113.5	7.1	1197	2	Q4RVM1_TETNG	Q4rvml tetraodon n
1402	113.5	7.1	2200	2	Q7YRF6_CANFA	Q7yrf6 canis famil
1403	113.5	7.1	4796	2	Q9W055_DROME	Q9w055 drosophila
1404	113	7.0	151	2	Q6JD93_9PERO	Q6jd93 leptomis pun
1405	113	7.0	151	2	Q6JD94_9PERO	Q6jd94 leptomis min
1406	113	7.0	302	2	Q7PN14_ANOGA	Q7pn14 anopheles g
1407	113	7.0	328	2	Q8UV42_BRARE	Q8uv42 brachydanio
1408	113	7.0	328	2	Q8UV99_BRARE	Q8uv99 brachydanio
1409	113	7.0	338	2	Q5GAK5_9VIRU	Q5gak5 grouper iri
1410	113	7.0	398	2	Q7Z3B9_HUMAN	Q7z3b9 homo sapien
1411	113	7.0	582	2	Q567S4_HUMAN	Q567s4 homo sapien
1412	113	7.0	626	1	MAC_HUMAN	P20916 homo sapien
1413	113	7.0	626	2	Q53ES7_HUMAN	Q53es7 homo sapien
1414	113	7.0	626	2	Q53HD1_HUMAN	Q53hd1 homo sapien
1415	113	7.0	626	2	Q5R4C0_PONPY	Q5r4c0 pongo pygma
1416	113	7.0	661	2	Q59GD9_HUMAN	Q59gd9 homo sapien
1417	113	7.0	705	2	Q63710_RATRT	Q63710 rattus ratt
1418	113	7.0	708	1	KRR2_HUMAN	Q6uw16 homo sapien

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP PROTEIN SEQUENCE OF 29-43.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [7]
RP INTERACTION WITH JAM3.
RX PubMed=11590146; DOI=10.1074/jbc.M105972200;
RA Arrate M.P., Rodriguez J.M., Tran T.M., Brock T.A., Cunningham S.A.;
RT "Cloning of human junctional adhesion molecule 3 (JAM3) and its
RT identification as the JAM2 counter-receptor.";
RL J. Biol. Chem. 276:45826-45832(2001).
RN [8]
RP REVIEW, AND NOMENCLATURE.
RX PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
RA Muller W.A.;
RT "Leukocyte-endothelial-cell interactions in leukocyte transmigration
RT and the inflammatory response.";
RL Trends Immunol. 24:327-334(2003).
CC -!- FUNCTION: May play a role in the processes of lymphocyte homing to
CC secondary lymphoid organs.
CC -!- SUBUNIT: Interacts with JAM3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC Localized at tight junctions of both epithelial and endothelial
CC cells (by similarity).
CC -!- TISSUE SPECIFICITY: Highest expression in the heart, placenta,
CC lung, foreskin and lymph node. Prominently expressed on high
CC endothelial venules, also present on the endothelia of other
CC vessels. Localized to the intercellular boundaries of high
CC endothelial cells.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF255910; AAF81223.1; -; mRNA.
CC EMBL; AY016009; AAG49022.1; -; mRNA.
CC EMBL; AY077698; AAL82538.1; -; mRNA.
CC EMBL; AY358361; AAQ88727.1; -; mRNA.
CC EMBL; BC017779; AAH17779.1; -; mRNA.
CC HSP; O88792; 1F97.

DR Ensembl; ENSG00000154721; Homo sapiens.
DR HGNC; HGNC:14686; JAM2.
DR H-InvDB; HIX0016038; -.
DR MIM; 606870; -.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016337; P:cell-cell adhesion; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Signal; Tight junction; Transmembrane.
FT SIGNAL 1 28
FT CHAIN 29 298
FT TOPO_DOM 29 238
FT TRANSMEM 239 259
FT TOPO_DOM 260 298
FT DOMAIN 32 127
FT DOMAIN 134 238
FT CARBOHYD 98 98
FT CARBOHYD 187 187
FT CARBOHYD 236 236
FT DISULFID 50 109
FT DISULFID 155 214
FT CONFLICT 270 270
FT CONFLICT 289 298
FT SEQUENCE 298 AA; 33207 MW; CA78E518E22DCAEE CRC64;
Query Match 91.9%; Score 1475; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.5e-11; Indels 0; Gaps 0;
Matches 288; Conservative 0; Mismatches 0;
QY 1 MARRSRHRLLLLLLYLVVALGYHKAYGSPAKDQOVTVAVYQEAAILACKTPKKTVSSR 60
DB 1 MARRSRHRLLLLLLYLVVALGYHKAYGSPAKDQOVTVAVYQEAAILACKTPKKTVSSR 60
QY 61 LEWKLGKRSVSVYVYQQTLOGDFKRAEMIDFNIRIKNTRSDAGKYRCEVSAPSQGN 120
DB 61 LEWKLGKRSVSVYVYQQTLOGDFKRAEMIDFNIRIKNTRSDAGKYRCEVSAPSQGN 120
QY 121 LSEDTVTLELVAVAPVPSCEVPSSALSGTVVSELRCODKEGNPAPEYTVFKDGIIRLLENPR 180
DB 121 LSEDTVTLELVAVAPVPSCEVPSSALSGTVVSELRCODKEGNPAPEYTVFKDGIIRLLENPR 180
QY 181 LGSQSTNSGYTNTKTGTQFNTVSKLDTGBYSCEARNSVGYRRCPGKMQVDDLNISGI 240
DB 181 LGSQSTNSGYTNTKTGTQFNTVSKLDTGBYSCEARNSVGYRRCPGKMQVDDLNISGI 240
QY 241 TAAVWVALVISVCGLGVCYAKRGYFYSKETSFKSNSSSKATTWSEN 288
DB 241 TAAVWVALVISVCGLGVCYAKRGYFYSKETSFKSNSSSKATTWSEN 288
RESULT 2
JAM2_MOUSE
ID JAM2_MOUSE STANDARD; PRT; 298 AA.
AC Q9J159; O8CSK9; O8CE95;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Junctional adhesion molecule B precursor (JAM-B) (Junctional adhesion
DE molecule 2) (Vascular endothelial junction-associated molecule) (VE-
DE JAM).
GN Name=Jam2; Synonyms=VeJam;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 29-33.

RC STRAIN=C57BL/6J; PubMed=10779521; DOI=10.1074/jbc.M003189200;
RX MEDLINE=20317114; PubMed=10779521; DOI=10.1074/jbc.M003189200;
RA Palmieri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RT "Vascular endothelial junction-associated molecule, a novel member of
FT the immunoglobulin superfamily, is localized to intercellular
RT boundaries of endothelial cells.";
RL J. Biol. Chem. 275:19139-19145 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=20489356; PubMed=11036763;
RA Aurrand-lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an emerging functional adhesion molecular
RT family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Head, Medulla oblongata, and Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RT Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Maceuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kurogaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Varadaraj R., Wagner L., Walstead C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boriss A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP REVIEW, AND NOMENCLATURE.

RX PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
RA Muller W.A.;
RT "Leukocyte-endothelial-cell interactions in leukocyte transmigration
RT and the inflammatory response.";
RL Trends Immunol. 24:327-334 (2003).
CC -1- FUNCTION: May play a role in the processes of lymphocyte homing to
CC secondary lymphoid organs (By similarity).
CC -1- SUBUNIT: Interacts with JAM3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC Localized at tight junctions of both epithelial and endothelial
CC cells.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF255911; AAF81224.1; -; mRNA.
DR EMBL; AJ291757; CAC20699.1; -; mRNA.
DR EMBL; AK010616; BAB27064.1; -; mRNA.
DR EMBL; AK013914; BAB29053.1; -; mRNA.
DR EMBL; AK028757; BAC26102.1; -; mRNA.
DR EMBL; AK078128; BAC37139.1; -; mRNA.
DR EMBL; BC028778; AAH28778.1; -; mRNA.
DR HSSP; O88792; 1P97.
DR Ensembl; ENSMUSG0000053062; Mus musculus.
DR MGI; MGI-1933820; Jam2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig C2.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Signal; Tight junction; Transmembrane.
FT SIGNAL 1 28
FT CHAIN 29 298
FT TOPO_DOM 29 236
FT TRANSMEM 237 257
FT TOPO_DOM 258 298
FT DOMAIN 32 128
FT DOMAIN 135 238
FT CARBOHYD 99 99
FT DISULFID 51 110
FT DISULFID 156 214
FT CONFLICT 133 133
FT CONFLICT 174 174
FT CONFLICT 183 183
FT SEQUENCE 298 AA; 33047 MW; 1124E0F07B6CF751 CRC64;
SQ
Query Match 73.0%; Score 1172; DB 1; Length 298;
Best Local Similarity 78.5%; Pred. No. 1.5e-86;
Matches 227; Conservative 25; Mismatches 35; Indels 2; Gaps 2;
Qy 1 MARRSRRLLLLLRLVYVALGYHKGAFSGAPKD-QQVTVAYVEQAILACKTPKKTSS 59
Db 1 MARRSPQGLMLLLHLVLYVALDYHKGAFSGAPKDRQEVTVIRFQAILACKTPKKTSS 60
Qy 60 RLSEWKKLGRSVFVYVYQQTLLQGGFKNAEMIDFNIRIKNTRSDAGKYRCEVAPSQGG 119
Db 61 RLSEWKKVQGVSLVYVYQALQGGFKDRAEMIDFNIRIKNTRSDAGKYRCEVAPSQGG 120

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Qy 120 NLEEDVTTLVLVAPVPSCEVPSSALSGTVVLRQCDKEGNPAPETWTFKDGIRLLENP 179
Db 121 NLQEDKMLVLVAPVAPVACEVPTSVMTGVSWSLRQCDKEGNPAPETWTFKDGTSLLGNP 180
Qy 180 RLQSQSTNSYTNNTKGTITQFTNTVSKLDTGEYSCBARNVGVRRCPGKRMQVDDLNIISG 239
Db 181 K-GGTHNNSYTNWTKSGIILQFNWIKMSDGEYCEARNVGVHRRCPGKRMQVDDLNIISG 239
Qy 240 IIAVVVVVALVISVCGLGVCYAKRGYFSKETSFOKNSSSSKATTWSEN 288
Db 240 IIAATVVVAFVISVCGLGTCYAKRGYFSKETSFOKNSPASKVTWSEN 288

RESULT 3
Q5ZJD1_CHICK
ID Q5ZJD1_CHICK PRELIMINARY; PRT; 243 AA.
AC Q5ZJD1;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypochemical protein.
GN ORFNames=RCJMB04.19d4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Brain;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezuabov Y., Zaim J.,
RA Fiedler P., Kuter S., Blagodatzi A., Kostovska D., Koter M.,
RA Flachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; A720503; CAG32162.1; -; mRNA.
DR InterPro; IPR007110; Ig-like.
DR DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_Like; 1.
KW Hypochemical protein; Immunoglobulin domain; Transmembrane.
SQ SEQUENCE 243 AA; 26738 MW; C1ASICCDIIIA4383 CRC64;

Query Match 37.3%; Score 598.5; DB 2; Length 243;
Best Local Similarity 48.4%; Pred. No. 3.3e-40;
Matches 134; Conservative 32; Mismatches 55; Indels 56; Gaps 7;

Qy 8 RLLLLLLRYLVALGTHKAYGFSAPKQDQVTVAYVEQAILACKTP-KKTVSSRLWKKL 66
Db 5 RLRLLLGLYGV-FCYHKVTGIAETDNKNVKAEEFKAILSCFKFSKMSLRIEWKKI 63
Qy 67 -GRSVSFVYVYQQLQDQFNKRAEMIDFNIRIKNVTSDAGKYRCEVSAPSEQQNLEEDT 125
Db 64 QSEVSFVYI-----NGEF----- 77
Qy 126 VTLEVLVAPVAPVPSCEVPSSALSGTVVLRQCDKEGNPAPETWTFKDGIRLLENPRLQS 185
Db 78 -----TVPTTFCVVPNSAMTGTVELSCKEAGSPPEYQWYKNGVALLKGTGTSAR 132
Qy 186 T-NSSYTMNTKTTLTQFTNTVSKLDTGEYSCBARNVGV-RRCPGKRMQVDDLNIISGIIAA 243
Db 133 TANITYTMNKSGLTIFNTVSKNDTGEYFCVASNGIGLPQKCSMKRMQVDDLNVSGIIAA 192
Qy 244 VVVVALVISVCGLGVCYAKRGYFSKETSFOKNSSS 280
Db 193 VVIVALVMALCGLVLYAOKGYFTKSSSQKNSOS 229

RESULT 4
Q9CWD9_MOUSE
ID Q5CWD9_MOUSE PRELIMINARY; PRT; 181 AA.
```

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AC Q9CWD9;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
DE clone:2410167M24 product:junction cell adhesion molecule 2, full
DE insert sequence (Mus musculus 9.5 days embryo parthenogenote cDNA,
DE RIKEN full-length enriched library, clone:BL30032E13 product:junction
DE cell adhesion molecule 2, full insert sequence).
GN Name=Jam2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuoka H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia C., Choithia C., Corbani L.E., Cousins S.,
RA Daila E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perce G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayase N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
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RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skoloka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=11739175; DOI=10.1182/blood.V98.13.3699;
RA Aurand-Lions M.A., Johnson-Leger C., Wong C., Du Pasquier L.,
RA Imhof B.A.;
RT "Heterogeneity of endothelial junctions is reflected by differential
RT expression and specific subcellular localization of the three JAM
RT family members.";
RL Blood 98:3699-3707 (2001).
RN [6]
RP REVIEW, AND NOMENCLATURE.
RX PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
RA Muller W.A.;
RT "Leukocyte-endothelial-cell interactions in leukocyte transmigration
RT and the inflammatory response.";
RL Trends Immunol. 24:327-334 (2003).
CC -!- FUNCTION: May participate in cell-cell adhesion distinct from
CC tight junctions.
CC -!- SUBUNIT: Interacts with JAM2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Endothelial cells.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AJ300304; CAC20704.1; -; mRNA.
CC EMBL; AK008187; BAB25519.1; -; mRNA.
CC EMBL; AK003326; BAB22715.1; -; mRNA.
CC EMBL; AK013156; BAB28683.1; -; mRNA.
CC EMBL; AK017692; BAC25526.1; -; mRNA.
CC EMBL; AK032833; BAC28049.1; -; mRNA.
CC EMBL; BC024357; AAH24357.1; -; mRNA.
CC HSSP; O88792; 1F97.
CC Ensembl; ENSMUSG00000031990; Mus musculus.
CC MGI; MGI:1933825; Jam3.

DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00408; IGc2; 2.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Glycoprotein; Immunoglobulin domain; Signal; Transmembrane.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 310 Junctional adhesion molecule C.
FT TOPO_DOM 30 241 Extracellular (Potential).
FT TRANSMEM 242 262 Potential.
FT TOPO_DOM 263 310 Cytoplasmic (Potential).
FT DOMAIN 35 137 Ig-like V-type.
FT DOMAIN 139 236 Ig-like C2-type.
FT CARBOHYD 104 104 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 192 192 N-linked (GlcNAc..) (Potential).
FT DISULFID 53 115 Potential.
FT DISULFID 160 219 Potential.
FT CONFLICT 44 44 H -> Q (in Ref. 3; BAB25519).
FT CONFLICT 172 172 S -> N (in Ref. 3; BAB25519).
FT CONFLICT 303 303 R -> K (in Ref. 3; BAB22715).
FT CONFLICT 306 307 SS -> IA (in Ref. 3; BAB22715).
SQ SEQUENCE 310 AA; 34838 MW; 4B92BCB51D0A4B0A CRC64;
Query Match 29.8%; Score 479; DB 1; Length 310;
Best Local Similarity 36.3%; Pred. No. 2.1e-30;
Matches 110; Conservative 62; Mismatches 109; Indels 22; Gaps 8;
QY 1 MARRSRHRL-----LLLLLYLVVLYGKAYGFSAPKQOVVTAVEYQEAAILAC-K 51
DB 3 LSRRLRLRLYARLPDFFLLLPFGCM-----EAVNLKSSNRNPVVH--EFESVLSUCII 55
QY 52 TPKTKVSSRLWKKL-GRSVSVVYVYQTLQGFQPKRAEMI-DFNIRIKNVTRSDAGKYRC 109
DB 56 TDSQTSDFRIEWKIQDQGTIVYVFNKIQGLAGRTDVGKTSLRINWVTRSDSAIYRC 115
QY 110 EVSAPSEQQNLEEDTTLVLVPAVPSCVPSVPSVPSVPSVPSVPSVPSVPSVPSVPSV 169
DB 116 EVVALNDR-KEVDEITIELIVQKFTVPCRIAPAAVPGVKATATLQCESEGYPRPHYSWY 174
QY 170 KDGIRLLENPRLGQSOSTSSSYTNKTKLTQNTVSKLDTGEVSCARNSVGYRRCPGKR 229
DB 175 RNDVPLPTDSRANPRFQSSSFVNSETGLVFNVAHVHKKDSGGQYCYIASNDAGARCEGD 234
QY 230 MQVDDLNISGIITAAVVALVISVGLGVYCAQRKGYFSKETSFKKSNSSSKATTMSENV 289
DB 235 MEVYDLNTAGIIGVVLVILVLAIVTMGICCAVRRGCF---ISSKQDGESYKSPGRHDGV 291
QY 290 QWL 292
DB 292 NYI 294
RESULT 6
JAM3 RAT STANDARD; PRT; 310 AA.
AC Q68FQ2;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Junctional adhesion molecule C precursor (JAM-C) (Junctional adhesion
DE molecule 3) (JAM-3).
GN Name=Jam3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Testis;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May participate in cell-cell adhesion distinct from
 CC tight junctions (By similarity).
 CC -1- SUBUNIT: Interacts with JAM2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily.
 CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
 CC domain.
 CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; BC079429; AAH79429.1; -; mRNA.
 DR Ensembl; ENSRNOG0000009149; Rattus norvegicus.
 DR RGD; 1303248; Jam3.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS00835; IG_LIKE; 2.
 KW Glycoprotein; Immunoglobulin domain; Signal; Transmembrane.
 FT SIGNAL 1 31
 FT CHAIN 32 310
 FT TOPO_DOM 32 310
 FT TRANSMEM 242 262
 FT TOPO_DOM 263 310
 FT DOMAIN 35 127
 FT DOMAIN 139 236
 FT CARBOHYD 104 104
 FT CARBOHYD 192 192
 FT DISULFID 53 115
 FT DISULFID 160 219
 FT SEQUENCE 310 AA; 34783 MW; BB0CAD5EE4D1D383B CRC64;
 Query Match 29.7%; Score 477; DB 1; Length 310;
 Best Local Similarity 37.0%; Pred. No. 3.1e-30;
 Matches 112; Conservative 59; Mismatches 110; Indels 22; Gaps 8;
 QY 1 MARRSRRL-----LALLRLVVLGVHAYGFSPKQDQVTVAVQERAILAC-K 51
 Db 3 LSRRLRLCARLPDPFLLLLRFGCVI-----EAVNLKSNRPVH--EFESVELSCII 55
 QY 52 TPKKTVSSRLWKKL-GRSVSVFYVYQOTLQDGFKNRAEMI-DFNIRIKNTVTRSDAGKYRC 109
 Db 56 TDSQTNDPRLEWKKIQDQGYTVYVFDNKIQGLAGRTDVGKTSRLRWVTRSDSAIYRC 115
 QY 110 EVGAPSPQGNLEBDTTLVLVAPVPSCEVPSVSSALSGTVELRCQDKGNPAPETWTF 169
 Db 116 EVVALANDR-KEVDLTLVQVFPVPCVPCVPCVPCVPCVPCVPCVPCVPCVPCVPCV 174
 QY 170 KDGIRLENLRLGQSNTSSVNTKGTLOFNTVSKLDTGEVSCERNVGVYRCPCGR 229
 Db 175 RNDVPLPTDPRANPRFQNSVFNSTGTILVFSVAVHKEDSGQYVCIAASNDAGAACRGQD 234
 QY 230 MQVDDLNISGIIAAVVVVALVISVCGVGVCAQKGYFSKTSFKNSSSSKATTSSENV 289
 Db 235 MEVVDNLNAGIIGGVVVLVAVITWIGICCAVERGCF---ISSKQDGEYSKPGKEGV 291
 QY 290 QWL 292
 Db 292 NYI 294

RESULT 7
 JAM3 HUMAN
 ID JAM3 HUMAN STANDARD; PRT; 310 AA.
 AC Q9BXG7; Q8WWL8; Q96FLJ;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Junctional adhesion molecule C precursor (JAM-C) (Junctional adhesion
 DE molecule 3) (JAM-3) (JAM-2).
 GN Names:JAM3; ORFNames=UNQ859/PRO1868;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, INTERACTION WITH JAM2, AND TISSUE SPECIFICITY.
 RC TISSUE=Brain;
 RX PubMed=11590146; DOI=10.1074/jbc.M105972200;
 RA Arrate M.P., Rodriguez J.M., Tran T.M., Brock T.A., Cunningham S.A.;
 RT "Cloning of human junctional adhesion molecule 3 (JAM3) and its
 RT identification as the JAM2 counter-receptor.";
 RL J. Biol. Chem. 276:45826-45832(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=11739175; DOI=10.1182/blood.V98.13.3699;
 RA Aurrand-Lions M.A., Johnson-Leger C., Wong C., Du Pasquier L.,
 RA Imhof B.A.;
 RT "Heterogeneity of endothelial junctions is reflected by differential
 RT expression and specific subcellular localization of the three JAM
 RT family members.";
 RL Blood 98:3699-3707(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=12208882; DOI=10.1084/jem.20020267;
 RA Santoso S., Sachs U.J.H., Kroll H., Linder M., Ruf A., Preissner K.T.,
 RA Chavakis T.;
 RT "The junctional adhesion molecule 3 (JAM-3) on human platelets is a
 RT counterreceptor for the leukocyte integrin Mac-1.";
 RL J. Exp. Med. 196:679-691(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
 RX MEDLINE=21945252; PubMed=11944976; DOI=10.1006/geno.2002.6742;
 RA Phillips H.M., Renforth G.L., Spalluto C., Hearn T., Curtis A.R.J.,
 RA Craven L., Havran B., Clement-Jones M., English C., Stumper O.,
 RA Salmon T., Hutchinson S., Jackson M.S., Wilson D.I.;
 RT "Narrowing the critical region within ilq24-qter for hypoplastic left
 RT heart and identification of a candidate gene, JAM3, expressed during
 RT cardiogenesis.";
 RL Genomics 79:475-478(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kikkawa E.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Kataura N., Sato K., Tanikawa K.,
 RA Yamazaki M., Ninomiya K., Iehibashi T., Yamaehita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotsu T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,


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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
MG79514 protein.
Name=MG79514;
Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
NCBI_TaxID=8364;
[1]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; and
RW Immunoglobulin domain.
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080901; AAH80901.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; IG_2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 291 AA; 31538 MW; D6A3115178E222A6 CRC64;

Query Match 27.7%; Score 445; DB 2; Length 291;
Best Local Similarity 35.0%; Pred. No. 1.1e-27;
Matches 103; Conservative 57; Mismatches 120; Indels 14; Gaps 6;

QY 1 MARRSRRLLLRLYLVALGVHAK-GFSAPKQQQVTVAVEQEAAILACKTPKKTSS 59
Db 1 MATASSNRGAVL--GLLCACLWTAAGVSTP--NPTITVKQATADLCTVTSDFTKS 56
QY 60 RLEWKKLGRSVS--FVYVQQTLOGDFKRAEMIDFNIRIKNVTSDAGKRCVSPASEQ 117
Db 57 RVEMKFNQNLFTFVYVYDGLTSLAYVNRATSVFQIILNQITSKDAGEVSCVTSVDSN 116
QY 118 GQNL-EDTWTLEVLVAPVSPVSSALSGITVVELRCQKGNPAPEYTWKDGIRLL 176
Db 117 GQTLVGEAKIQLLVIVAPQPMARVPTNVTGSAVELRCVETQGPPTFTYQNKAPMP 176
QY 177 ENPLRGSQSTSSVTMTKGTQFNVTSLKDTGEYCEARNVGYRCPCPKQMOVDLN 236
Db 177 PNPO-----NATITIDNTGLVKFRAVASDSGDYCKANSEGRQVSAIRVMVDVN 230
QY 237 ISGIIAAVWVALVYVCGLVGCYQAKRGYFSKTSFKQNSSSKATMTSENQ 290
Db 231 VGGIVAAVVLILALIGLWYATSRGYLDKKGKVIYQSPSETRSDKNFQ 284

RESULT 9
Q640C0_XENLA PRELIMINARY; PRT; 296 AA.
ID Q640C0;
AC Q640C0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE LOC398627 protein (Fragment).
GN Name=LOC398627;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
[1]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391 (2002).
[2]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; and
RW Immunoglobulin domain.
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
NUCLEOTIDE SEQUENCE.
RP TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082710; AAH82710.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_c2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON TER 1
SQ SEQUENCE 296 AA; 32269 MW; 2EF4953AB840A15C CRC64;

Query Match 27.4%; Score 439.5; DB 2; Length 296;
Best Local Similarity 35.4%; Pred. No. 3.2e-27;
Matches 95; Conservative 55; Mismatches 101; Indels 17; Gaps 5;

QY 28 GFSAPKQQQVTVAVEQEAAILACKTPKKTSSSLEWKKLGR--SVSPVYVQQTLOGDFKN 85
Db 34 GVTPAP--DPTITVKEGSDPLRCSTSYSDYINPRVEMKFNQDQETSFVFDGSLTASYKD 91
QY 86 RAEMIDFNIRIKNVTSDAGKRCVSPASEQ---GQNL-EDTWTLEVLVAPVSPCEVP 142
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Db      92  RATSYPQGIKLNQVTRKDAAGEYCEVTSYTGKVLG-----EAKIQLOVIVAPGTPVAQVP 147
Qy      143  SSALSGTVVVELRCQDKGPNAPYTFWFKDGIIRLLENPRLGSGSTNSYTNKTKGTLOFN 202
Db      148  SSARTGSVAELMCVETQGFPLFTFTWYHN-----NSPMQAKSQNSTYTDPTNTGLVKFA 201
Qy      203  TVSKLDTGYSCEARNVSVGRPCGRKMOVDLNLISGIILAAVVVVVALVSVCGLGVCYQAQ 262
Db      202  SVGTSDSGEYCKATNSQGEQSAIVRMVDKVNNGVIAAUVVILLIALLGFLWLFAY 261
Qy      263  RKGYFSKTSFQKSNSSSKATTMSENVQ 290
Db      262  SRGYLDRKGNKKVIYQSPSETRSDKNFQ 289

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AC       Q7SYQ7_XENLA PRELIMINARY;          PRT;          300 AA.
DT       01-OCT-2003 (TReMBLrel. 25, Created)
DT       01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT       01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE       LOC398627 protein (Fragment).
GN       Name=LOC398627;
OS       Xenopus laevis (African clawed frog).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC       Xenopodinae; Xenopus; Xenopus.
OX       NCBI_TaxID=8355;
RN       [1]
RP       NUCLEOTIDE SEQUENCE.
RC       TISSUE=Whole;
RX       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA       Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA       Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA       Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA       Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA       Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA       Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA       Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA       Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA       Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA       Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA       Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA       Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA       Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA       Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA       Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA       Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA       Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT       "Generation and initial analysis of more than 15,000 full-length human
RT       and mouse cDNA sequences."
RL       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN       [2]
RP       NUCLEOTIDE SEQUENCE.
RC       TISSUE=Whole;
RX       MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA       Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA       Richardson P.;
RT       "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT       Initiative."
RL       Dev. Dyn. 225:384-391(2002).
RN       [3]
RP       NUCLEOTIDE SEQUENCE.
RC       TISSUE=Whole;
RA       Klein S., Strausberg R.;
RL       Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR       EMBL; BC054305; AAH54305.1; -; mRNA.
DR       HSSP; O88792; 1F97.
DR       InterPro; IPR007110; Ig-like.
DR       InterPro; IPR003598; Ig_c2.
DR       SMART; SM00408; IG2; 1.
DR       PROSITE; PSS0835; IG_LIKE; 2.
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FT      NON TER      1
SQ      SEQUENCE      300 AA; 32858 MH; 02BC49DC74E271D4 CRC64;

Query Match      27.4%; Score 439.5; DB 2; Length 300;
Best Local Similarity 35.4%; Pred. No. 3.3e-27;
Matches 95; Conservative 55; Mismatches 101; Indels 17; Gaps 5;

Qy      28  GFSAPKDDQVVTAVEYQEAAILACKTPKKTVSRLWKKLGR--SVSFVYVYQQTLOGDFKN 85
Db      38  GVTAP--DFTITVKGSDSPDLRCSTYSYDINRVEWKFVVKQOETSFVFDGSLTASYKD 95
Qy      86  RAEMIDFNIRIKNVTSRDAGKYRCEVSAPSEQ---GQNLSEEDVTILEVLVAPVPSCEVP 142
Db      96  RATSYPQGIKLNQVTRKDAAGEYCEVTSYTGKVLG-----EAKIQLOVIVAPGTPVAQVP 151
Qy      143  SSALSGTVVVELRCQDKGPNAPYTFWFKDGIIRLLENPRLGSGSTNSYTNKTKGTLOFN 202
Db      152  SSARTGSVAELMCVETQGFPLFTFTWYHN-----NSPMQAKSQNSTYTDPTNTGLVKFA 205
Qy      203  TVSKLDTGYSCEARNVSVGRPCGRKMOVDLNLISGIILAAVVVVVALVSVCGLGVCYQAQ 262
Db      206  SVGTSDSGEYCKATNSQGEQSAIVRMVDKVNNGVIAAUVVILLIALLGFLWLFAY 265
Qy      263  RKGYFSKTSFQKSNSSSKATTMSENVQ 290
Db      266  SRGYLDRKGNKKVIYQSPSETRSDKNFQ 293

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DT       01-JUN-2003 (TReMBLrel. 24, Created)
DT       01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT       01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE       MGC53721 protein.
OS       Xenopus laevis (African clawed frog).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC       Xenopodinae; Xenopus; Xenopus.
OX       NCBI_TaxID=8355;
RN       [1]
RP       NUCLEOTIDE SEQUENCE.
RC       TISSUE=Embryo;
RX       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA       Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA       Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA       Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA       Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA       Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA       Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA       Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA       Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA       Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA       Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA       Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA       Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA       Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA       Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA       Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA       Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA       Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT       "Generation and initial analysis of more than 15,000 full-length human
RT       and mouse cDNA sequences."
RL       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN       [2]
RP       NUCLEOTIDE SEQUENCE.
RC       TISSUE=Embryo;
RX       MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA       Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA       Richardson P.;
RT       "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT       Initiative."
RL       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RA Norin A.J., Hartwig J., Salifu M.O., Markell M.S., Babinska A.,
RA Ehrlich Y.H., Kornecki E.;
RT "Cloning of the human platelet P11 receptor: a cell adhesion molecule
RT member of the immunoglobulin superfamily involved in platelet
RT aggregation.";
RL Blood 95:2600-2609(2000).
RN [3]
RN NUCLEOTIDE SEQUENCE [MRNA], AND SUBCELLULAR LOCATION.
RX PubMed=11171323;
RA Naik U.P., Naik M.U., Eckfeld K., Martin-DeLeon P., Sychala J.;
RT "Characterization and chromosomal localization of JAM-1, a platelet
RT receptor for a stimulatory monoclonal antibody.";
RL J. Cell Sci. 114:539-547(2001).
RN [4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed=11171323;
RA Naik U.P., Naik M.U., Eckfeld K., Martin-DeLeon P., Sychala J.;
RT "Characterization and chromosomal localization of JAM-1, a platelet
RT receptor for a stimulatory monoclonal antibody.";
RL J. Cell Sci. 114:539-547(2001).
RN [4]
RN TISSUE=Brain;
RX MEDLINE=21154917; PubMed=1230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glasel S.,
RA Ansoerge W., Boecher M., Blocker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Pouetka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN [5]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [6]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rutterfield Y.S.N., Krzywinski M.I., Skalka U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RN PROTEIN SEQUENCE OF 28-103 AND 123-130, AND N-GLYCOSYLATION.
RX PubMed=7646439;
RA Naik U.P., Ehrlich Y.H., Kornecki E.;
RT "Mechanisms of platelet activation by a stimulatory antibody: cross-
RT linking of a novel platelet receptor for monoclonal antibody P11 with
RT the P2 gamma RII receptor";
RL Biochem. J. 310:155-162(1995).

[8]
PROTEIN SEQUENCE OF 28-42.
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Hensel W.J.;
"Signal peptide prediction based on analysis of experimentally
verified cleavage sites";
Protein Sci. 13:2819-2824(2004).
[9]
PROTEIN SEQUENCE OF 28-39.
TISSUE=Platelet;
MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
Gevaert K., Goethals M., Martens L., Van Damme J., Staess A.,
Thomas G.R., Vandekerckhove J.;
"Exploring proteomes and analyzing protein processing by mass
spectrometric identification of sorted N-terminal peptides.";
Nat. Biotechnol. 21:566-569(2003).
[10]
INTERACTION WITH MPDZ.
PubMed=11489913; DOI=10.1083/jcb.200103047;
Itoh M., Sasaki H., Furuse M., Ozaki H., Kita T., Tsukita S.;
"Junctional adhesion molecule (JAM) binds to PAR-3: a possible
mechanism for the recruitment of PAR-3 to tight junctions.";
J. Cell Biol. 154:491-497(2001).
[11]
REVIEW, AND NOMENCLATURE.
PubMed=12810109; DOI=10.1016/S1471-4906(03)00117-0;
Muller W.A.;
"Leukocyte-endothelial-cell interactions in leukocyte transmigration
and the inflammatory response.";
Trends Immunol. 24:327-334(2003).
-1- FUNCTION: Seems to plays a role in epithelial tight junction
formation. Appears early in primordial forms of cell junctions and
recruits PAR3. The association of the PAR3-PARD3 complex may
prevent the interaction of PAR3 with JAM1, thereby preventing
tight junction assembly (By similarity). Plays a role in
regulating monocyte transmigration involved in integrity of
epithelial barrier. Involved in platelet activation.
-1- SUBUNIT: Interacts with the first PDZ domain of PAR3. The
association between PAR3 and PAR6B probably disrupts this
interaction (By similarity). Interacts with the ninth PDZ domain
of MPDZ.
-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
Localized at tight junctions of both epithelial and endothelial
cells.
-1- PTM: N-Glycosylated.
-1- SIMILARITY: Belongs to the immunoglobulin superfamily.
-1- SIMILARITY: Contains 2 Ig-like V-type (immunoglobulin-like)
domains.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; AF111713; AAD42050.1; -; mRNA.
EMBL; AF207907; AAF22829.1; -; mRNA.
EMBL; AF172398; AAD48877.1; -; mRNA.
EMBL; AL136649; CAB66584.1; -; mRNA.
EMBL; AY358896; AAO89255.1; -; mRNA.
EMBL; BC001533; AAH01533.1; -; mRNA.
FIR; AS9406; S56749.
PDB; 1NHQ; X-ray; A/B=27-233.
Ensembl; ENSG00000158769; Homo sapiens.
HGNC; HGNC:14685; F11R.
MIM; 605721; -.
GO; GO:0005911; C:intercellular junction; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; Ig; 1.
PROSITE; PS50835; IG_LIKE; 2.
3D-structure; Direct protein sequencing; Glycoprotein; Transmembrane.
Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 17:42:09 ; Search time 24 seconds
(without alignments)
1074.784 Million cell updates/sec

Title: US-10-785-607C-9

Perfect score: 1605

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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3: /cgn2_6/ptodata/1/iaa/H COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/PCBUS COMB.pap:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1605	100.0	312	2	US-09-254-465A-9
2	1605	100.0	312	2	US-09-907-794A-64
3	1605	100.0	312	2	US-09-905-125A-64
4	1605	100.0	312	2	US-09-902-775A-64
5	1605	100.0	312	2	US-09-906-700-64
6	1605	100.0	312	2	US-09-903-603A-64
7	1605	100.0	312	2	US-09-904-920A-64
8	1605	100.0	312	2	US-09-909-064-64
9	1605	100.0	312	2	US-09-905-381A-64
10	1605	100.0	312	2	US-09-906-618-64
11	1605	100.0	312	2	US-09-953-499-9
12	1605	100.0	312	2	US-09-906-646-64
13	1605	100.0	312	2	US-09-904-462-64
14	1605	100.0	312	2	US-09-902-736A-64
15	1605	100.0	312	2	US-09-906-722A-64
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17	1465	91.3	298	2	US-09-852-797-76
18	1465	91.3	298	2	US-09-853-161-76
19	1465	91.3	298	2	US-10-058-993-76
20	461.5	28.8	310	2	US-09-907-794A-423
21	461.5	28.8	310	2	US-09-905-125A-423
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25	461.5	28.8	310	2	US-09-904-920A-423
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31	461.5	28.8	310	2	US-09-902-736A-423	Sequence 423, App
32	461.5	28.8	310	2	US-10-033-301-20	Sequence 20, Appl
33	461.5	28.8	310	2	US-09-906-722A-423	Sequence 423, App
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35	404	25.2	299	2	US-09-188-930-331	Sequence 331, App
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46	404	25.2	299	2	US-09-904-920A-119	Sequence 119, App
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58	394	24.5	300	2	US-09-953-499-25	Sequence 25, Appl
59	394	24.5	300	2	US-09-254-465A-10	Sequence 10, Appl
60	394	24.5	300	2	US-09-397-243D-12	Sequence 12, Appl
61	394	24.5	300	2	US-09-953-499-10	Sequence 10, Appl
62	273.5	17.0	205	2	US-09-462-270-4	Sequence 4, Appli
63	238	14.8	270	2	US-09-254-465A-24	Sequence 24, Appl
64	238	14.8	270	2	US-09-953-499-24	Sequence 24, Appl
65	238	14.8	273	2	US-09-254-465A-26	Sequence 26, Appl
66	238	14.8	273	2	US-09-953-499-26	Sequence 26, Appl
67	238	14.8	319	1	US-08-597-495B-22	Sequence 22, Appl
68	238	14.8	319	2	US-09-068-051A-22	Sequence 22, Appl
69	238	14.8	319	2	US-09-336-536-67	Sequence 67, Appl
70	238	14.8	319	2	US-09-254-465A-6	Sequence 6, Appli
71	238	14.8	319	2	US-09-953-499-6	Sequence 6, Appli
72	234.5	14.6	316	2	US-09-397-243D-13	Sequence 13, Appl
73	224.5	14.0	133	2	US-09-397-243D-4	Sequence 4, Appli
74	222	13.8	318	2	US-09-068-051A-32	Sequence 32, Appl
75	211.5	13.2	387	2	US-09-175-928-2	Sequence 2, Appli
76	210	13.1	330	1	US-08-979-424-1	Sequence 1, Appli
77	210	13.1	330	2	US-09-907-794A-39	Sequence 39, Appl
78	210	13.1	330	2	US-09-905-125A-39	Sequence 39, Appl
79	210	13.1	330	2	US-09-902-775A-39	Sequence 39, Appl
80	210	13.1	330	2	US-09-906-700-39	Sequence 39, Appl
81	210	13.1	330	2	US-09-903-603A-39	Sequence 39, Appl
82	210	13.1	330	2	US-09-904-920A-39	Sequence 39, Appl
83	210	13.1	330	2	US-09-909-064-39	Sequence 39, Appl
84	210	13.1	330	2	US-09-905-381A-39	Sequence 39, Appl
85	210	13.1	330	2	US-09-906-618-39	Sequence 39, Appl
86	210	13.1	330	2	US-09-906-646-39	Sequence 39, Appl
87	210	13.1	330	2	US-09-904-462-39	Sequence 39, Appl
88	210	13.1	330	2	US-09-902-736A-39	Sequence 39, Appl
89	210	13.1	330	2	US-09-906-722A-39	Sequence 39, Appl
90	207.5	12.9	334	2	US-09-336-536-39	Sequence 39, Appl
91	203	12.6	370	2	US-09-336-536-28	Sequence 28, Appl
92	202	12.6	76	2	US-09-397-243D-11	Sequence 11, Appl
93	200	12.5	365	2	US-09-336-536-40	Sequence 40, Appl
94	199.5	12.4	341	2	US-09-336-536-29	Sequence 29, Appl
95	199	12.4	383	2	US-09-949-016-11050	Sequence 11050, A
96	198.5	12.4	352	2	US-08-991-181-505	Sequence 505, App
97	198.5	12.4	352	2	US-09-990-444-505	Sequence 505, App
98	198.5	12.4	352	2	US-09-997-333-505	Sequence 505, App
99	198.5	12.4	352	2	US-09-992-598-505	Sequence 505, App
100	198.5	12.4	365	1	US-08-979-424-3	Sequence 3, Appli

101	198.5	12.4	365	2	US-09-272-496-2	Sequence 2, Appli	174	150	9.3	1501	1	US-08-716-679-3	Sequence 3, Appli
102	198.5	12.4	365	2	US-09-949-016-6064	Sequence 6064, Ap	175	149.5	9.3	349	2	US-09-924-103-4	Sequence 4, Appli
103	194.5	12.1	365	2	US-08-928-383B-2	Sequence 2, Appli	176	149.5	9.3	637	2	US-09-569-611C-35	Sequence 35, Appl
104	193.5	12.1	317	2	US-10-104-047-3036	Sequence 3036, Ap	177	148.5	9.3	1381	2	US-09-540-245A-16	Sequence 16, Appl
105	189	11.8	249	2	US-09-336-536-42	Sequence 42, Appl	178	148.5	9.3	1381	2	US-10-289-776-16	Sequence 16, Appl
106	188	11.7	365	2	US-08-928-383B-23	Sequence 23, Appl	179	148	9.2	344	1	US-08-602-725-34	Sequence 34, Appl
107	188	11.7	365	2	US-08-928-383B-24	Sequence 24, Appl	180	148	9.2	357	2	US-09-949-016-9074	Sequence 9074, Ap
108	188	11.7	365	2	US-09-899-634C-4	Sequence 4, Appli	181	148	9.2	363	2	US-09-949-016-11040	Sequence 11040, A
109	185	11.5	365	2	US-08-928-383B-26	Sequence 26, Appl	182	148	9.2	365	2	US-09-949-016-9075	Sequence 9075, Ap
110	183.5	11.4	246	2	US-09-336-536-31	Sequence 31, Appl	183	148	9.2	371	2	US-09-949-016-9073	Sequence 6, Appli
111	181.5	11.3	261	2	US-09-899-634C-2	Sequence 2, Appli	184	148	9.2	407	2	US-08-753-007A-6	Sequence 6, Appli
112	178.5	11.1	466	2	US-09-604-107A-8	Sequence 8, Appli	185	148	9.2	407	2	US-09-398-496-6	Sequence 6, Appli
113	171.5	10.7	5518	2	US-09-953-096-2	Sequence 2, Appli	186	148	9.2	469	2	US-08-753-007A-8	Sequence 8, Appli
114	168.5	10.5	329	2	US-10-104-047-3709	Sequence 3709, Ap	187	148	9.2	469	2	US-09-398-496-8	Sequence 8, Appli
115	166.5	10.4	442	2	US-09-778-510-20	Sequence 20, Appl	188	148	9.2	647	2	US-08-753-007A-32	Sequence 32, Appl
116	166.5	10.4	442	2	US-09-930-803-1	Sequence 1, Appli	189	148	9.2	647	2	US-09-398-496-32	Sequence 32, Appl
117	166.5	10.4	4126	2	US-09-953-096-4	Sequence 4, Appli	190	146.5	9.1	1101	1	US-08-986-485-2	Sequence 2, Appli
118	163.5	10.2	373	2	US-09-991-181-503	Sequence 503, App	191	146	9.1	464	1	US-08-602-725-32	Sequence 32, Appl
119	163.5	10.2	373	2	US-09-999-833A-59	Sequence 59, Appl	192	146	9.1	464	2	US-09-949-016-6116	Sequence 6116, Ap
120	163.5	10.2	373	2	US-09-990-444-503	Sequence 503, App	193	146	9.1	464	2	US-09-949-016-7525	Sequence 7525, Ap
121	163.5	10.2	373	2	US-09-997-333-503	Sequence 503, App	194	146	9.1	1194	2	US-10-191-029-10	Sequence 10, Appl
122	163.5	10.2	373	2	US-09-992-598-503	Sequence 503, App	195	145.5	9.1	1651	2	US-09-540-245A-18	Sequence 18, Appl
123	163.5	10.2	373	2	US-10-020-445A-59	Sequence 59, Appl	196	145.5	9.1	1651	2	US-10-289-776-18	Sequence 18, Appl
124	163.5	10.2	440	2	US-09-866-028-61	Sequence 61, Appl	197	145.5	9.1	1709	2	US-09-949-016-10503	Sequence 10503, A
125	163.5	10.2	440	2	US-09-944-457-61	Sequence 61, Appl	198	145	9.0	181	2	US-08-753-007A-4	Sequence 4, Appli
126	163.5	10.2	440	2	US-09-945-584-61	Sequence 61, Appl	199	145	9.0	181	2	US-09-398-496-4	Sequence 4, Appli
127	163.5	10.2	440	2	US-09-944-584-61	Sequence 61, Appl	200	145	9.0	605	2	US-08-753-007A-2	Sequence 2, Appli
128	163.5	10.2	440	2	US-09-945-587-61	Sequence 61, Appl	201	145	9.0	605	2	US-09-398-496-2	Sequence 2, Appli
129	162	10.1	805	2	US-08-985-526-34	Sequence 34, Appl	202	145	9.0	1395	2	US-09-540-245A-15	Sequence 15, Appl
130	162	10.1	806	1	US-08-443-861-5	Sequence 5, Appli	203	145	9.0	1395	2	US-10-289-776-15	Sequence 15, Appl
131	162	10.1	806	1	US-08-193-829B-5	Sequence 5, Appli	204	144.5	9.0	1297	2	US-09-540-245A-17	Sequence 17, Appl
132	162	10.1	806	2	US-09-766-678-5	Sequence 5, Appli	205	144.5	9.0	1297	2	US-10-289-776-17	Sequence 17, Appl
133	162	10.1	1367	1	US-07-813-593-4	Sequence 4, Appli	206	144	9.0	1911	1	US-08-348-006B-5	Sequence 5, Appli
134	162	10.1	1367	1	US-07-977-451-6	Sequence 6, Appli	207	144	9.0	1911	1	US-08-800-825A-5	Sequence 5, Appli
135	162	10.1	1367	1	US-07-946-507-4	Sequence 4, Appli	208	144	9.0	1911	4	US-09-158-657-5	Sequence 5, Appli
136	162	10.1	1367	1	US-08-252-517-6	Sequence 6, Appli	209	144	9.0	1911	4	PCT-US94-10166-5	Sequence 5, Appli
137	162	10.1	1367	1	US-07-906-397A-6	Sequence 6, Appli	210	143.5	8.9	398	2	US-09-778-510-6	Sequence 6, Appli
138	162	10.1	1367	1	US-08-601-891-6	Sequence 6, Appli	211	143.5	8.9	398	2	US-09-907-794A-84	Sequence 84, Appl
139	162	10.1	1367	1	US-08-443-861-2	Sequence 2, Appli	212	143.5	8.9	398	2	US-09-905-125A-84	Sequence 84, Appl
140	162	10.1	1367	1	US-09-021-324-6	Sequence 6, Appli	213	143.5	8.9	398	2	US-09-902-775A-84	Sequence 84, Appl
141	162	10.1	1367	2	US-08-193-829B-2	Sequence 2, Appli	214	143.5	8.9	398	2	US-09-906-700-84	Sequence 84, Appl
142	162	10.1	1367	2	US-09-872-136B-6	Sequence 6, Appli	215	143.5	8.9	398	2	US-09-903-603A-84	Sequence 84, Appl
143	162	10.1	1367	2	US-09-766-678-2	Sequence 2, Appli	216	143.5	8.9	398	2	US-09-904-920A-84	Sequence 84, Appl
144	162	10.1	1367	2	US-09-919-408A-6	Sequence 6, Appli	217	143.5	8.9	398	2	US-09-909-064-84	Sequence 84, Appl
145	162	10.1	1367	4	PCT-US92-02750-8	Sequence 8, Appli	218	143.5	8.9	398	2	US-09-905-381A-84	Sequence 84, Appl
146	162	10.1	1367	4	PCT-US92-05401-6	Sequence 6, Appli	219	143.5	8.9	398	2	US-09-906-618-84	Sequence 84, Appl
147	162	10.1	1367	4	PCT-US92-09893-6	Sequence 6, Appli	220	143.5	8.9	398	2	US-09-906-646-84	Sequence 84, Appl
148	161.5	10.1	423	2	US-09-778-510-22	Sequence 22, Appl	221	143.5	8.9	398	2	US-09-904-462-84	Sequence 84, Appl
149	161	10.0	365	2	US-09-949-016-7591	Sequence 7591, Ap	222	143.5	8.9	398	2	US-09-902-736A-84	Sequence 84, Appl
150	160	10.0	837	2	US-09-949-016-6515	Sequence 6515, Ap	223	143.5	8.9	398	2	US-09-906-722A-84	Sequence 84, Appl
151	159	9.9	819	2	US-09-949-016-11044	Sequence 11044, A	224	143.5	8.9	432	2	US-09-778-510-2	Sequence 2, Appli
152	157	9.8	330	1	US-08-525-864A-4	Sequence 4, Appli	225	143	8.9	642	1	US-08-217-299-1	Sequence 1, Appli
153	157	9.8	754	1	US-08-525-864A-2	Sequence 2, Appli	226	143	8.9	698	1	US-08-602-725-36	Sequence 36, Appl
154	156.5	9.8	421	1	US-08-659-984A-1	Sequence 1, Appli	227	143	8.9	702	2	US-09-949-016-6484	Sequence 6484, Ap
155	156.5	9.8	421	2	US-08-660-531-1	Sequence 1, Appli	228	143	8.9	734	1	US-08-389-459A-17	Sequence 17, Appl
156	156.5	9.8	421	2	US-09-404-578-1	Sequence 1, Appli	229	143	8.9	734	2	US-08-389-459A-17	Sequence 17, Appl
157	156.5	9.8	444	1	US-08-659-984A-5	Sequence 5, Appli	230	143	8.9	740	2	US-09-949-016-8168	Sequence 8168, Ap
158	156.5	9.8	444	2	US-08-660-531-5	Sequence 5, Appli	231	143	8.9	1115	2	US-10-012-231A-58	Sequence 58, Appl
159	156.5	9.8	444	2	US-09-404-578-5	Sequence 5, Appli	232	143	8.9	1115	2	US-10-015-389A-58	Sequence 58, Appl
160	156	9.7	306	2	US-10-191-029-12	Sequence 12, Appl	233	143	8.9	1115	2	US-10-006-768A-58	Sequence 58, Appl
161	155.5	9.7	421	2	US-09-569-611C-36	Sequence 36, Appl	234	143	8.9	1115	2	US-10-015-671A-58	Sequence 58, Appl
162	155	9.7	298	2	US-09-864-675-4	Sequence 4, Appli	235	143	8.9	1115	2	US-10-015-393A-58	Sequence 58, Appl
163	155	9.7	330	2	US-09-864-675-2	Sequence 2, Appli	236	143	8.9	1115	2	US-10-011-833A-58	Sequence 58, Appl
164	154.5	9.6	4391	2	US-10-006-011A-2	Sequence 2, Appli	237	143	8.9	1115	2	US-10-006-041A-58	Sequence 58, Appl
165	152.5	9.5	398	2	US-09-778-510-4	Sequence 4, Appli	238	143	8.9	1115	2	US-10-012-064A-58	Sequence 328, App
166	152	9.5	615	1	US-08-752-307B-9	Sequence 9, Appli	239	142	8.8	847	2	US-09-949-002-328	Sequence 328, App
167	152	9.5	615	2	US-09-707-802-9	Sequence 9, Appli	240	142	8.8	862	2	US-09-949-002-427	Sequence 427, App
168	152	9.5	615	2	US-09-991-326-9	Sequence 9, Appli	241	140.5	8.8	946	4	PCT-US95-08493-13	Sequence 13, Appl
169	151.5	9.4	588	2	US-09-949-016-10547	Sequence 10547, A	242	140	8.7	501	1	US-08-408-095-31	Sequence 31, Appl
170	151.5	9.4	848	2	US-09-787-443-44	Sequence 44, Appl	243	139.5	8.7	826	2	US-09-877-730-16	Sequence 16, Appl
171	150.5	9.4	296	2	US-09-667-135-36	Sequence 36, Appl	244	139.5	8.7	904	2	US-09-877-730-6	Sequence 6, Appli
172	150	9.3	198	2	US-09-569-611C-34	Sequence 34, Appl	245	139.5	8.7	907	2	US-09-877-730-20	Sequence 20, Appl
173	150	9.3	1501	1	US-08-447-464-3	Sequence 3, Appli	246	139.5	8.7	985	2	US-09-877-730-10	Sequence 10, Appl

247	139.5	8.7	991	2	US-09-877-730-12	Sequence 12, Appl	320	132.5	8.3	1356	2	US-09-483-539-2	Sequence 2, Appl
248	139.5	8.7	1069	2	US-09-877-730-2	Sequence 2, Appl	321	132.5	8.3	1356	2	US-09-949-016-6198	Sequence 6198, Ap
249	139.5	8.7	1072	2	US-09-877-730-18	Sequence 18, Appl	322	132.5	8.3	1356	2	US-10-100-405A-2	Sequence 2, Appl
250	139.5	8.7	1150	2	US-09-877-730-8	Sequence 8, Appl	323	132.5	8.3	1356	2	US-10-022-939-2	Sequence 2, Appl
251	139	8.7	477	1	US-08-359-705B-4	Sequence 4, Appl	324	132.5	8.3	1456	2	US-09-949-016-9853	Sequence 9853, Ap
252	139	8.7	477	1	US-08-286-846A-4	Sequence 4, Appl	325	132	8.2	1070	2	US-09-961-403-3	Sequence 3, Appl
253	139	8.7	477	1	US-08-457-880A-4	Sequence 4, Appl	326	131.5	8.2	303	2	US-09-651-200-23	Sequence 23, Appl
254	139	8.7	477	1	US-08-444-622A-4	Sequence 4, Appl	327	131.5	8.2	303	2	US-09-441-411-15	Sequence 15, Appl
255	139	8.7	477	2	US-08-942-562-4	Sequence 4, Appl	328	131.5	8.2	303	2	US-09-441-411-20	Sequence 20, Appl
256	139	8.7	477	2	US-08-156-923-4	Sequence 4, Appl	329	131.5	8.2	309	1	US-08-456-104-4	Sequence 4, Appl
257	139	8.7	650	2	US-10-104-047-3395	Sequence 3395, Ap	330	131.5	8.2	309	2	US-08-479-744A-23	Sequence 23, Appl
258	139	8.7	822	1	US-08-359-705B-2	Sequence 2, Appl	331	131.5	8.2	309	2	US-08-280-757B-23	Sequence 23, Appl
259	139	8.7	822	1	US-08-286-846A-2	Sequence 2, Appl	332	131.5	8.2	309	2	US-08-205-697A-21	Sequence 21, Appl
260	139	8.7	822	1	US-08-457-880A-2	Sequence 2, Appl	333	131.5	8.2	309	2	US-08-702-525-21	Sequence 21, Appl
261	139	8.7	822	2	US-08-444-622A-2	Sequence 2, Appl	334	131.5	8.2	309	2	US-09-651-200-22	Sequence 22, Appl
262	139	8.7	822	2	US-08-942-562-2	Sequence 2, Appl	335	131.5	8.2	309	2	US-09-667-135-33	Sequence 33, Appl
263	139	8.7	822	2	US-09-156-923-2	Sequence 2, Appl	336	131.5	8.2	309	2	US-09-425-762-23	Sequence 23, Appl
264	139	8.7	822	2	US-09-949-016-6698	Sequence 6698, Ap	337	131.5	8.2	309	2	US-09-837-867A-21	Sequence 21, Appl
265	139	8.7	847	1	US-08-286-305A-5	Sequence 5, Appl	338	131.5	8.2	309	2	US-09-206-132-4	Sequence 4, Appl
266	139	8.7	847	1	US-08-441-104A-5	Sequence 5, Appl	339	131.5	8.2	309	2	US-09-441-411-13	Sequence 13, Appl
267	139	8.7	847	1	US-08-440-816A-5	Sequence 5, Appl	340	131.5	8.2	309	2	US-09-441-411-18	Sequence 18, Appl
268	139	8.7	847	2	US-08-417-381A-5	Sequence 5, Appl	341	131.5	8.2	309	2	US-09-441-411-24	Sequence 24, Appl
269	138.5	8.6	983	2	US-08-412-554A-2	Sequence 2, Appl	342	131.5	8.2	309	2	US-09-425-516-23	Sequence 23, Appl
270	137	8.5	321	6	5169835-17	Patent No. 5169835	343	131.5	8.2	309	4	FCT-US95-02576-21	Sequence 21, Appl
271	136.5	8.5	146	2	US-09-270-767-33187	Sequence 33187, A	344	131.5	8.2	313	2	US-09-700-397-4	Sequence 4, Appl
272	136.5	8.5	821	1	US-08-339-578-2	Sequence 2, Appl	345	131.5	8.2	314	2	US-08-205-697A-13	Sequence 13, Appl
273	136	8.5	95	2	US-08-928-383B-18	Sequence 18, Appl	346	131.5	8.2	314	2	US-08-702-525-13	Sequence 13, Appl
274	136	8.5	500	2	US-10-012-231A-148	Sequence 148, App	347	131.5	8.2	314	2	US-09-837-867A-13	Sequence 13, Appl
275	136	8.5	500	2	US-10-015-389A-148	Sequence 148, App	348	131.5	8.2	314	2	US-09-441-411-14	Sequence 14, Appl
276	136	8.5	500	2	US-10-006-768A-148	Sequence 148, App	349	131.5	8.2	314	2	US-09-441-411-19	Sequence 19, Appl
277	136	8.5	500	2	US-10-015-671A-148	Sequence 148, App	350	131.5	8.2	314	4	FCT-US95-02576-13	Sequence 13, Appl
278	136	8.5	500	2	US-10-015-393A-148	Sequence 148, App	351	131.5	8.2	344	2	US-09-700-397-3	Sequence 3, Appl
279	136	8.5	500	2	US-10-011-833A-148	Sequence 148, App	352	131.5	8.2	344	2	US-09-999-833A-523	Sequence 523, App
280	136	8.5	500	2	US-10-006-041A-148	Sequence 148, App	353	131.5	8.2	344	2	US-10-020-445A-523	Sequence 523, App
281	136	8.5	500	2	US-10-012-064A-148	Sequence 148, App	354	131.5	8.2	356	2	US-09-441-411-11	Sequence 11, Appl
282	135	8.4	338	2	US-09-976-594-404	Sequence 404, App	355	131.5	8.2	356	2	US-09-441-411-12	Sequence 12, Appl
283	134.5	8.4	290	2	US-09-910-174B-8	Sequence 8, Appl	356	131.5	8.2	356	2	US-09-441-411-16	Sequence 16, Appl
284	134.5	8.4	290	2	US-09-620-461-8	Sequence 8, Appl	357	131.5	8.2	356	2	US-09-441-411-17	Sequence 17, Appl
285	134.5	8.4	290	2	US-08-451-291-1	Sequence 1, Appl	358	131.5	8.2	356	1	US-08-232-538-13	Sequence 13, Appl
286	134.5	8.4	290	2	US-08-645-069-4	Sequence 4, Appl	359	131.5	8.2	668	1	US-08-786-164-13	Sequence 13, Appl
287	134.5	8.4	290	2	US-09-915-789A-17	Sequence 17, Appl	360	131.5	8.2	788	1	US-08-232-538-15	Sequence 15, Appl
288	134.5	8.4	290	2	US-09-644-934-4	Sequence 4, Appl	361	131.5	8.2	788	1	US-08-786-164-15	Sequence 15, Appl
289	134.5	8.4	322	2	US-09-667-135-2	Sequence 2, Appl	362	131	8.2	252	2	US-09-270-767-44627	Sequence 44627, A
290	134.5	8.4	322	2	US-09-910-174B-29	Sequence 29, Appl	363	131	8.2	271	2	US-09-818-247-4	Sequence 4, Appl
291	134.5	8.4	322	2	US-09-620-461-29	Sequence 29, Appl	364	130.5	8.1	191	2	US-09-270-767-33678	Sequence 33678, A
292	134.5	8.4	483	2	US-09-949-016-8574	Sequence 8574, Ap	365	130.5	8.1	191	2	US-09-270-767-48895	Sequence 48895, A
293	134	8.3	338	1	US-08-414-657D-60	Sequence 60, Appl	366	130.5	8.1	434	2	US-09-540-245A-19	Sequence 19, Appl
294	134	8.3	338	2	US-09-135-080-8	Sequence 8, Appl	367	130.5	8.1	434	2	US-10-289-776-19	Sequence 19, Appl
295	134	8.3	771	2	US-08-434-000A-8	Sequence 8, Appl	368	129.5	8.1	252	1	US-08-414-657D-56	Sequence 56, Appl
296	134	8.3	771	2	US-09-312-157-8	Sequence 8, Appl	369	129.5	8.1	252	1	US-08-414-657D-57	Sequence 57, Appl
297	134	8.3	771	2	US-08-717-888-8	Sequence 8, Appl	370	129.5	8.1	287	1	US-08-414-657D-48	Sequence 48, Appl
298	134	8.3	868	1	US-08-374-834-1	Sequence 1, Appl	371	129.5	8.1	287	1	US-08-414-657D-49	Sequence 49, Appl
299	134	8.3	868	1	US-08-644-271-1	Sequence 1, Appl	372	129.5	8.1	304	1	US-08-414-657D-44	Sequence 44, Appl
300	134	8.3	868	2	US-09-077-955-1	Sequence 1, Appl	373	129.5	8.1	308	1	US-08-414-657D-46	Sequence 46, Appl
301	134	8.3	868	2	US-10-016-283-1	Sequence 1, Appl	374	129.5	8.1	315	1	US-08-414-657D-47	Sequence 47, Appl
302	134	8.3	1617	2	US-09-784-358-16	Sequence 16, Appl	375	129.5	8.1	325	1	US-08-414-657D-2	Sequence 2, Appl
303	134	8.3	1691	2	US-09-784-358-2	Sequence 2, Appl	376	129.5	8.1	325	1	US-08-414-657D-41	Sequence 41, Appl
304	133.5	8.3	278	2	US-09-270-767-42034	Sequence 42034, A	377	129.5	8.1	325	2	US-09-135-080-2	Sequence 2, Appl
305	133.5	8.3	347	2	US-09-667-135-4	Sequence 4, Appl	378	129	8.0	769	2	US-08-434-000A-10	Sequence 10, Appl
306	133	8.3	310	1	US-08-414-657D-45	Sequence 45, Appl	379	129	8.0	769	2	US-09-312-157-10	Sequence 10, Appl
307	133	8.3	338	1	US-08-414-657D-42	Sequence 42, Appl	380	129	8.0	769	2	US-09-717-888-10	Sequence 10, Appl
308	133	8.3	338	1	US-08-414-657D-43	Sequence 43, Appl	381	129	8.0	769	2	US-09-818-247-3	Sequence 3, Appl
309	133	8.3	338	2	US-09-135-080-4	Sequence 4, Appl	382	128.5	8.0	757	2	US-09-818-247-2	Sequence 2, Appl
310	133	8.3	894	2	US-09-949-016-10605	Sequence 10605, A	383	128.5	8.0	1953	2	US-09-917-254-92	Sequence 92, Appl
311	132.5	8.3	764	2	US-09-142-955B-14	Sequence 14, Appl	384	128	8.0	245	2	US-09-645-069-2	Sequence 2, Appl
312	132.5	8.3	767	1	US-08-874-678-2	Sequence 2, Appl	385	128	8.0	245	2	US-09-644-934-2	Sequence 2, Appl
313	132.5	8.3	767	2	US-08-643-839-2	Sequence 2, Appl	386	128	8.0	869	1	US-08-374-834-16	Sequence 16, Appl
314	132.5	8.3	767	2	US-09-348-886-2	Sequence 2, Appl	387	128	8.0	869	1	US-08-644-271-29	Sequence 29, Appl
315	132.5	8.3	767	2	US-10-105-901A-2	Sequence 2, Appl	388	128	8.0	869	2	US-09-077-955-33	Sequence 33, Appl
316	132.5	8.3	801	2	US-09-383-630-6	Sequence 6, Appl	389	128	8.0	869	2	US-09-715-249-8	Sequence 8, Appl
317	132.5	8.3	1356	1	US-08-810-116-8	Sequence 8, Appl	390	128	8.0	869	2	US-10-016-283-33	Sequence 33, Appl
318	132.5	8.3	1356	1	US-07-930-548A-8	Sequence 8, Appl	391	128	8.0	1363	2	US-09-375-248-19	Sequence 19, Appl
319	132.5	8.3	1356	2	US-09-098-707A-2	Sequence 2, Appl	392	127	7.9	504	2	US-09-949-016-7020	Sequence 7020, Ap

393	127	7.9	504	2	US-09-991-181-119	Sequence 119, App	466	124	7.7	612	1	US-08-752-307B-11	Sequence 11, Appl
394	127	7.9	504	2	US-09-990-444-119	Sequence 119, App	467	124	7.7	612	2	US-09-707-802-11	Sequence 11, Appl
395	127	7.9	504	2	US-09-997-333-119	Sequence 119, App	468	124	7.7	612	2	US-09-991-326-11	Sequence 28, Appl
396	127	7.9	504	2	US-09-992-598-119	Sequence 119, App	469	124	7.7	1268	2	US-08-506-296B-28	Sequence 2, Appl
397	127	7.9	511	2	US-09-949-016-10054	Sequence 10054, A	470	123.5	7.7	59	2	US-09-324-541-2	Sequence 2, Appl
398	126.5	7.9	306	1	US-08-147-772-4	Sequence 4, Appl	471	123.5	7.7	282	2	US-10-198-053-623	Sequence 623, App
399	126.5	7.9	306	1	US-08-456-104-8	Sequence 8, Appl	472	123.5	7.7	299	2	US-09-651-200-15	Sequence 15, Appl
400	126.5	7.9	306	1	US-08-101-624-25	Sequence 25, Appl	473	123.5	7.7	322	2	US-09-383-586-33	Sequence 33, Appl
401	126.5	7.9	306	1	US-08-153-262-4	Sequence 4, Appl	474	123.5	7.7	322	2	US-09-823-038A-33	Sequence 33, Appl
402	126.5	7.9	306	2	US-08-479-744A-31	Sequence 31, Appl	475	123.5	7.7	419	6	5169835-2	Patent No. 5169835
403	126.5	7.9	306	2	US-08-280-757B-31	Sequence 31, Appl	476	123.5	7.7	757	2	US-08-434-000A-6	Sequence 6, Appl
404	126.5	7.9	306	2	US-09-159-135-4	Sequence 4, Appl	477	123.5	7.7	757	2	US-09-312-157-6	Sequence 6, Appl
405	126.5	7.9	306	2	US-08-205-697A-17	Sequence 17, Appl	478	123.5	7.7	757	2	US-09-717-888-6	Sequence 6, Appl
406	126.5	7.9	306	2	US-08-702-525-17	Sequence 17, Appl	479	123	7.7	302	2	US-09-915-789A-18	Sequence 18, Appl
407	126.5	7.9	306	2	US-09-450-798-4	Sequence 4, Appl	480	123	7.7	309	2	US-09-667-135-6	Sequence 6, Appl
408	126.5	7.9	306	2	US-09-651-200-17	Sequence 17, Appl	481	123	7.7	309	2	US-09-910-174B-7	Sequence 7, Appl
409	126.5	7.9	306	2	US-09-667-135-35	Sequence 35, Appl	482	123	7.7	309	2	US-09-620-461-7	Sequence 7, Appl
410	126.5	7.9	306	2	US-09-425-762-31	Sequence 31, Appl	483	123	7.7	315	2	US-09-910-174B-28	Sequence 28, Appl
411	126.5	7.9	306	2	US-09-837-867A-17	Sequence 17, Appl	484	123	7.7	315	2	US-09-620-461-28	Sequence 28, Appl
412	126.5	7.9	306	2	US-08-453-386A-4	Sequence 4, Appl	485	123	7.7	526	1	US-08-471-570-4	Sequence 4, Appl
413	126.5	7.9	306	2	US-09-206-132-8	Sequence 8, Appl	486	123	7.7	607	1	US-08-752-307B-12	Sequence 12, Appl
414	126.5	7.9	306	2	US-09-425-516-31	Sequence 31, Appl	487	123	7.7	607	2	US-09-707-802-12	Sequence 12, Appl
415	126.5	7.9	306	4	PCT-US95-02576-17	Sequence 17, Appl	488	123	7.7	607	2	US-09-991-326-12	Sequence 12, Appl
416	126.5	7.9	1447	2	US-09-041-886-25	Sequence 25, Appl	489	123	7.7	652	1	US-08-471-570-10	Sequence 10, Appl
417	126.5	7.9	1447	4	PCT-US94-05277-2	Sequence 2, Appl	490	123	7.7	1091	2	US-08-986-485-5	Sequence 5, Appl
418	126	7.9	758	1	US-08-874-678-1	Sequence 1, Appl	491	122.5	7.6	1311	1	US-08-340-011-5	Sequence 5, Appl
419	126	7.9	758	2	US-08-643-839-1	Sequence 1, Appl	492	122.5	7.6	1311	2	US-08-901-710-5	Sequence 5, Appl
420	126	7.9	758	2	US-09-051-363-24	Sequence 24, Appl	493	122.5	7.6	1311	2	US-09-169-079-5	Sequence 5, Appl
421	126	7.9	758	2	US-09-348-886-1	Sequence 1, Appl	494	122.5	7.6	1571	2	US-08-956-991-11	Sequence 11, Appl
422	126	7.9	758	2	US-10-105-501A-1	Sequence 1, Appl	495	122.5	7.6	1910	2	US-08-956-991-2	Sequence 2, Appl
423	126	7.9	780	1	US-08-232-538-14	Sequence 14, Appl	496	122	7.6	732	2	US-09-818-247-5	Sequence 5, Appl
424	126	7.9	780	1	US-08-786-164-14	Sequence 14, Appl	497	122	7.6	820	2	US-09-620-561-1	Sequence 1, Appl
425	126	7.9	1338	2	US-08-750-141A-3	Sequence 3, Appl	498	121.5	7.6	304	2	US-09-646-561-2	Sequence 2, Appl
426	126	7.9	1338	2	US-09-119-014D-6	Sequence 6, Appl	499	121.5	7.6	424	6	5169835-6	Patent No. 5169835
427	126	7.9	2596	2	US-09-548-073B-6	Sequence 6, Appl	500	121.5	7.6	828	1	US-08-261-304-2	Sequence 2, Appl
428	125.5	7.8	227	2	US-09-205-258-947	Sequence 947, App	501	121	7.5	61	2	US-09-513-999C-6595	Sequence 6595, Ap
429	125.5	7.8	227	2	US-10-004-860-947	Sequence 947, App	502	121	7.5	351	4	PCT-US93-05703-2	Sequence 2, Appl
430	125.5	7.8	230	6	5169835-13	Patent No. 5169835	503	121	7.5	351	4	US-09-667-135-28	Sequence 28, Appl
431	125.5	7.8	282	2	US-09-404-879A-393	Sequence 393, App	504	121	7.5	622	2	US-09-499-846-2	Sequence 2, Appl
432	125.5	7.8	282	2	US-09-667-857-393	Sequence 393, App	505	121	7.5	643	1	US-08-471-570-6	Sequence 6, Appl
433	125.5	7.8	282	2	US-10-198-053-393	Sequence 393, App	506	121	7.5	769	1	US-08-471-570-8	Sequence 8, Appl
434	125.5	7.8	282	2	US-09-915-789A-5	Sequence 5, Appl	507	121	7.5	820	1	US-07-921-807B-3	Sequence 3, Appl
435	125.5	7.8	282	2	US-09-991-181-291	Sequence 291, App	508	121	7.5	820	1	US-08-441-944A-3	Sequence 3, Appl
436	125.5	7.8	282	2	US-09-929-769-8	Sequence 8, Appl	509	121	7.5	820	2	US-08-166-717D-6	Sequence 6, Appl
437	125.5	7.8	282	2	US-09-990-444-291	Sequence 291, App	510	121	7.5	820	2	US-08-439-992A-1	Sequence 1, Appl
438	125.5	7.8	282	2	US-09-997-333-291	Sequence 291, App	511	120.5	7.5	821	2	US-08-451-822A-13	Sequence 13, Appl
439	125.5	7.8	282	2	US-09-992-598-291	Sequence 291, App	512	120.5	7.5	821	2	US-08-323-430-13	Sequence 13, Appl
440	125.5	7.8	282	2	US-09-927-271-393	Sequence 393, App	513	120	7.5	321	2	US-09-254-465A-2	Sequence 2, Appl
441	125.5	7.8	309	2	US-09-404-879A-392	Sequence 392, App	514	120	7.5	321	2	US-09-953-499-2	Sequence 2, Appl
442	125.5	7.8	309	2	US-09-667-857-392	Sequence 392, App	515	120	7.5	321	2	US-09-999-833A-52	Sequence 52, Appl
443	125.5	7.8	309	2	US-10-198-053-392	Sequence 392, App	516	120	7.5	321	2	US-10-020-445A-52	Sequence 52, Appl
444	125.5	7.8	309	2	US-09-827-271-392	Sequence 392, App	517	120	7.5	609	2	US-09-949-016-7747	Sequence 7747, Ap
445	125.5	7.8	558	2	US-09-667-135-31	Sequence 31, Appl	518	120	7.5	609	2	US-09-949-016-7748	Sequence 7748, Ap
446	125.5	7.8	795	2	US-09-949-016-7119	Sequence 7119, Ap	519	120	7.5	609	2	US-09-949-016-7750	Sequence 7750, Ap
447	125.5	7.8	806	2	US-09-383-630-3	Sequence 3, Appl	520	120	7.5	609	2	US-09-949-016-7751	Sequence 7751, Ap
448	125	7.8	478	4	PCT-US95-08493-15	Sequence 15, Appl	521	120	7.5	609	2	US-09-949-016-7752	Sequence 7752, Ap
449	125	7.8	833	2	US-09-949-016-11496	Sequence 11496, A	522	120	7.5	609	2	US-09-949-016-7753	Sequence 7753, Ap
450	125	7.8	860	4	PCT-US95-08493-19	Sequence 19, Appl	523	120	7.5	609	2	US-09-949-016-7754	Sequence 7754, Ap
451	125	7.8	868	4	PCT-US95-08493-21	Sequence 21, Appl	524	120	7.5	817	1	US-07-640-029-2	Sequence 2, Appl
452	125	7.8	1180	2	US-09-949-016-6577	Sequence 6577, Ap	525	120	7.5	822	1	US-07-997-133-1	Sequence 1, Appl
453	124.5	7.8	1241	2	US-09-040-774-2	Sequence 2, Appl	526	120	7.5	822	1	US-07-921-807B-4	Sequence 4, Appl
454	124.5	7.8	1665	2	US-09-858-664A-2	Sequence 2, Appl	527	120	7.5	822	1	US-08-459-296-2	Sequence 2, Appl
455	124.5	7.8	1665	2	US-10-274-978-2	Sequence 2, Appl	528	120	7.5	822	1	US-08-441-944A-4	Sequence 4, Appl
456	124.5	7.8	1665	2	US-10-697-263-2	Sequence 2, Appl	529	120	7.5	822	1	US-08-451-822A-12	Sequence 12, Appl
457	124	7.7	462	1	US-08-752-307B-7	Sequence 7, Appl	530	120	7.5	822	1	US-08-439-992A-2	Sequence 2, Appl
458	124	7.7	462	2	US-09-707-802-7	Sequence 7, Appl	531	120	7.5	822	2	US-08-323-430-12	Sequence 12, Appl
459	124	7.7	462	2	US-09-991-326-7	Sequence 7, Appl	532	120	7.5	822	2	US-09-620-561-2	Sequence 2, Appl
460	124	7.7	465	1	US-08-752-307B-5	Sequence 5, Appl	533	120	7.5	1018	1	US-08-452-052-2	Sequence 2, Appl
461	124	7.7	465	2	US-09-707-802-5	Sequence 5, Appl	534	120	7.5	1745	2	US-09-800-729-89	Sequence 89, Appl
462	124	7.7	465	2	US-09-991-326-5	Sequence 5, Appl	535	119.5	7.4	227	2	US-09-915-789A-19	Sequence 19, Appl
463	124	7.7	596	1	US-08-752-307B-13	Sequence 13, Appl	536	119.5	7.4	816	1	US-07-640-029-1	Sequence 1, Appl
464	124	7.7	596	2	US-09-707-802-13	Sequence 13, Appl	537	119.5	7.4	1610	2	US-09-548-473B-4	Sequence 4, Appl
465	124	7.7	596	2	US-09-991-326-13	Sequence 13, Appl	538	119.5	7.4	1610	2	US-09-548-473B-4	Sequence 4, Appl

539	119	7.4	291	2	US-10-027-736A-19	Sequence 19, Appl	612	117	7.3	292	2	US-09-800-729-175	Sequence 175, Appl
540	119	7.4	302	2	US-09-877-730-14	Sequence 14, Appl	613	117	7.3	316	2	US-10-027-736A-17	Sequence 17, Appl
541	119	7.4	315	2	US-09-949-016-11121	Sequence 11121, A	614	117	7.3	816	2	US-09-949-016-8119	Sequence 8119, Ap
542	119	7.4	315	2	US-09-949-016-11122	Sequence 11122, A	615	116.5	7.3	63	2	US-09-397-243D-8	Sequence 8, Appl
543	119	7.4	380	2	US-08-759-628-4	Sequence 4, Appl	616	116.5	7.3	63	2	US-09-397-243D-10	Sequence 10, Appl
544	119	7.4	440	2	US-08-759-628-4	Sequence 4, Appl	617	116.5	7.3	212	2	US-09-949-016-10458	Sequence 10458, A
545	119	7.4	985	2	US-09-999-833A-211	Sequence 211, App	618	116.5	7.3	623	2	US-09-949-016-11206	Sequence 11206, A
546	119	7.4	985	2	US-10-020-445A-211	Sequence 211, App	619	116.5	7.3	636	2	US-09-653-961-2	Sequence 2, Appl
547	119	7.4	1018	1	US-08-408-093-6	Sequence 6, Appl	620	116.5	7.3	746	2	US-08-434-000A-4	Sequence 4, Appl
548	119	7.4	1018	1	US-08-408-420A-6	Sequence 6, Appl	621	116.5	7.3	746	2	US-09-312-157-4	Sequence 4, Appl
549	119	7.4	1018	1	US-08-714-901-6	Sequence 6, Appl	622	116.5	7.3	746	2	US-09-717-888-4	Sequence 4, Appl
550	119	7.4	1018	1	US-08-714-901-6	Sequence 6, Appl	623	116.5	7.3	746	2	US-09-949-016-6254	Sequence 6254, Ap
551	119	7.4	1044	2	US-09-949-016-10321	Sequence 10321, A	624	116.5	7.3	764	2	US-09-818-247-1	Sequence 1, Appl
552	118.5	7.4	252	2	US-10-027-736A-68	Sequence 68, Appl	625	116.5	7.3	1123	2	US-09-949-016-6230	Sequence 6230, Ap
553	118.5	7.4	294	2	US-10-027-736A-18	Sequence 18, Appl	626	116.5	7.3	1128	2	US-09-949-016-7522	Sequence 7522, Ap
554	118.5	7.4	307	1	US-08-332-562A-83	Sequence 83, Appl	627	116.5	7.3	1266	2	US-08-506-296B-4	Sequence 4, Appl
555	118.5	7.4	315	2	US-09-949-016-7014	Sequence 7014, Ap	628	116	7.2	310	2	US-10-027-736A-15	Sequence 15, Appl
556	118.5	7.4	317	2	US-10-027-736A-16	Sequence 16, Appl	629	116	7.2	332	2	US-09-991-181-517	Sequence 517, App
557	118.5	7.4	355	1	US-08-471-570-14	Sequence 14, Appl	630	116	7.2	332	2	US-09-999-833A-216	Sequence 216, App
558	118.5	7.4	471	2	US-09-949-016-9042	Sequence 9042, Ap	631	116	7.2	332	2	US-09-990-444-517	Sequence 517, App
559	118.5	7.4	471	2	US-09-949-016-9043	Sequence 9043, Ap	632	116	7.2	332	2	US-09-997-333-517	Sequence 517, App
560	118.5	7.4	471	2	US-09-949-016-9044	Sequence 9044, Ap	633	116	7.2	332	2	US-09-992-598-517	Sequence 517, App
561	118.5	7.4	471	2	US-09-949-016-9045	Sequence 9045, Ap	634	116	7.2	332	2	US-10-020-445A-216	Sequence 216, App
562	118.5	7.4	471	2	US-09-949-016-9046	Sequence 9046, Ap	635	116	7.2	1509	2	US-09-677-046A-2	Sequence 2, Appl
563	118.5	7.4	471	2	US-09-949-016-9047	Sequence 9047, Ap	636	115.5	7.2	63	2	US-10-037-417-128	Sequence 128, App
564	118.5	7.4	471	2	US-09-949-016-9048	Sequence 9048, Ap	637	115.5	7.2	288	2	US-09-651-200-14	Sequence 14, Appl
565	118.5	7.4	471	2	US-09-949-016-9049	Sequence 9049, Ap	638	115.5	7.2	320	2	US-08-205-697A-2	Sequence 2, Appl
566	118.5	7.4	471	2	US-09-949-016-9050	Sequence 9050, Ap	639	115.5	7.2	320	2	US-08-702-525-2	Sequence 2, Appl
567	118.5	7.4	471	2	US-09-949-016-9051	Sequence 9051, Ap	640	115.5	7.2	320	2	US-09-837-867A-2	Sequence 2, Appl
568	118.5	7.4	646	2	US-09-949-016-6728	Sequence 6728, Ap	641	115.5	7.2	320	4	PCT-US95-02576-2	Sequence 2, Appl
569	118.5	7.4	646	2	US-09-949-016-6728	Sequence 4, Appl	642	115.5	7.2	513	2	US-09-910-174B-18	Sequence 18, Appl
570	118.5	7.4	735	4	PCT-US93-00031-13	Sequence 13, Appl	643	115.5	7.2	513	2	US-09-620-461-18	Sequence 18, Appl
571	118.5	7.4	736	4	PCT-US93-00031-15	Sequence 15, Appl	644	115.5	7.2	514	2	US-09-949-016-11380	Sequence 11380, A
572	118.5	7.4	739	2	US-08-482-073-6	Sequence 6, Appl	645	115.5	7.2	517	2	US-09-723-368-4	Sequence 4, Appl
573	118.5	7.4	739	4	PCT-US93-00031-9	Sequence 9, Appl	646	115.5	7.2	608	2	US-09-095-385-4	Sequence 4, Appl
574	118.5	7.4	740	4	PCT-US93-00031-17	Sequence 17, Appl	647	115.5	7.2	662	1	US-08-261-304-7	Sequence 7, Appl
575	118.5	7.4	1059	2	US-09-907-794A-290	Sequence 290, App	648	115.5	7.2	888	1	US-08-445-640-35	Sequence 35, Appl
576	118.5	7.4	1059	2	US-09-905-125A-290	Sequence 290, App	649	115.5	7.2	888	2	US-08-170-558-35	Sequence 35, Appl
577	118.5	7.4	1059	2	US-09-902-775A-290	Sequence 290, App	650	115.5	7.2	888	2	US-08-447-314-35	Sequence 35, Appl
578	118.5	7.4	1059	2	US-09-906-700-290	Sequence 290, App	651	115.5	7.2	888	2	US-08-445-461-35	Sequence 35, Appl
579	118.5	7.4	1059	2	US-09-903-603A-290	Sequence 290, App	652	115.5	7.2	888	2	US-09-223-490-35	Sequence 35, Appl
580	118.5	7.4	1059	2	US-09-904-920A-290	Sequence 290, App	653	115	7.2	220	2	US-09-915-789A-23	Sequence 23, Appl
581	118.5	7.4	1059	2	US-09-905-361A-290	Sequence 290, App	654	115	7.2	261	2	US-09-270-767-381898	Sequence 381898, A
582	118.5	7.4	1059	2	US-09-905-381A-290	Sequence 290, App	655	115	7.2	261	2	US-09-270-767-48115	Sequence 48115, A
583	118.5	7.4	1059	2	US-09-906-618-290	Sequence 290, App	656	115	7.2	354	6	5169835-4	Patent No. 5169835
584	118.5	7.4	1059	2	US-09-906-646-290	Sequence 290, App	657	115	7.2	549	2	US-09-858-664A-5	Sequence 5, Appl
585	118.5	7.4	1059	2	US-09-904-462-290	Sequence 290, App	658	115	7.2	549	2	US-10-274-378-6	Sequence 6, Appl
586	118.5	7.4	1059	2	US-09-902-736A-290	Sequence 290, App	659	115	7.2	549	2	US-10-697-263-6	Sequence 6, Appl
587	118.5	7.4	1059	2	US-09-906-722A-290	Sequence 290, App	660	115	7.2	549	2	US-08-428-926-5	Sequence 5, Appl
588	118.5	7.4	1119	2	US-09-907-794A-294	Sequence 294, App	661	115	7.2	602	1	US-08-428-927-5	Sequence 5, Appl
589	118.5	7.4	1119	2	US-09-905-125A-294	Sequence 294, App	662	115	7.2	602	1	US-08-428-298-5	Sequence 5, Appl
590	118.5	7.4	1119	2	US-09-902-775A-294	Sequence 294, App	663	115	7.2	602	1	US-08-339-517-5	Sequence 5, Appl
591	118.5	7.4	1119	2	US-09-906-700-294	Sequence 294, App	664	115	7.2	611	1	US-08-752-307B-10	Sequence 10, Appl
592	118.5	7.4	1119	2	US-09-903-603A-294	Sequence 294, App	665	115	7.2	611	2	US-09-707-802-10	Sequence 10, Appl
593	118.5	7.4	1119	2	US-09-904-920A-294	Sequence 294, App	666	115	7.2	611	2	US-09-991-326-10	Sequence 10, Appl
594	118.5	7.4	1119	2	US-09-909-064-294	Sequence 294, App	667	115	7.2	1253	2	US-08-506-296B-14	Sequence 14, Appl
595	118.5	7.4	1119	2	US-09-905-381A-294	Sequence 294, App	668	115	7.2	1298	1	US-08-222-616-33	Sequence 33, Appl
596	118.5	7.4	1119	2	US-09-906-618-294	Sequence 294, App	669	115	7.2	1298	1	US-08-340-011-2	Sequence 2, Appl
597	118.5	7.4	1119	2	US-09-906-646-294	Sequence 294, App	670	115	7.2	1298	2	US-08-901-710-2	Sequence 2, Appl
598	118.5	7.4	1119	2	US-09-904-462-294	Sequence 294, App	671	115	7.2	1298	2	US-08-446-648-33	Sequence 33, Appl
599	118.5	7.4	1119	2	US-09-902-736A-294	Sequence 294, App	672	115	7.2	1298	2	US-09-982-610-33	Sequence 33, Appl
600	118.5	7.4	1119	2	US-09-906-722A-294	Sequence 294, App	673	115	7.2	1298	2	US-09-169-079-2	Sequence 2, Appl
601	118.5	7.4	1248	2	US-09-949-016-10595	Sequence 10595, A	674	115	7.2	1298	4	PCT-US95-04228-33	Sequence 33, Appl
602	118.5	7.4	1248	2	US-09-949-016-10596	Sequence 10596, A	675	115	7.2	1362	1	US-08-874-678-33	Sequence 33, Appl
603	118	7.4	272	1	US-08-282-951-6	Sequence 6, Appl	676	115	7.2	1362	2	US-08-643-839-33	Sequence 33, Appl
604	118	7.4	337	1	US-08-442-043A-18	Sequence 18, Appl	677	115	7.2	1362	2	US-09-348-886-33	Sequence 33, Appl
605	118	7.4	337	2	US-09-560-639-6	Sequence 6, Appl	678	115	7.2	1362	2	US-10-105-901A-33	Sequence 33, Appl
606	118	7.4	337	2	US-08-441-893A-18	Sequence 18, Appl	679	115	7.2	1363	1	US-08-340-011-4	Sequence 4, Appl
607	118	7.4	342	2	US-09-032-337-41	Sequence 41, Appl	680	115	7.2	1363	2	US-08-901-710-4	Sequence 4, Appl
608	118	7.4	567	2	US-09-560-639-7	Sequence 7, Appl	681	115	7.2	1363	2	US-09-375-248-2	Sequence 2, Appl
609	118	7.4	567	2	US-09-173-151A-24	Sequence 24, Appl	682	115	7.2	1363	2	US-09-169-079-4	Sequence 4, Appl
610	118	7.4	567	2	US-09-032-337-39	Sequence 39, Appl	683	115	7.2	1368	1	US-08-874-678-34	Sequence 34, Appl
611	117	7.3	241	2	US-09-915-789A-11	Sequence 11, Appl	684	115	7.2	1368	2	US-08-643-839-34	Sequence 34, Appl

685	115	7.2	1368	2	US-09-348-886-34	Sequence 34, Appl	758	112.5	7.0	635	2	US-08-467-602-365	Sequence 365, App
686	115	7.2	1368	2	US-10-105-901A-34	Sequence 34, Appl	759	112.5	7.0	635	2	US-08-411-295F-291	Sequence 291, App
687	114.5	7.1	1363	1	US-08-874-678-32	Sequence 32, Appl	760	112.5	7.0	782	2	US-09-684-708A-21	Sequence 21, Appl
688	114.5	7.1	1363	1	US-08-643-839-32	Sequence 32, Appl	761	112.5	7.0	818	2	US-08-470-335-234	Sequence 234, App
689	114.5	7.1	1363	2	US-09-348-886-32	Sequence 32, Appl	762	112.5	7.0	818	2	US-08-467-602-321	Sequence 321, App
690	114.5	7.1	1363	2	US-10-105-901A-32	Sequence 32, Appl	763	112.5	7.0	818	2	US-08-411-295F-247	Sequence 247, App
691	114	7.1	1369	2	US-09-949-016-8059	Sequence 8059, Ap	764	112.5	7.0	852	2	US-08-467-602-363	Sequence 363, App
692	114	7.1	1260	2	US-08-506-296B-21	Sequence 21, Appl	765	112.5	7.0	852	2	US-08-411-295F-289	Sequence 289, App
693	113.5	7.1	1282	2	US-10-027-736A-66	Sequence 66, Appl	766	112.5	7.0	865	2	US-08-470-335-235	Sequence 235, App
694	113.5	7.1	386	2	US-08-467-602-281	Sequence 281, App	767	112.5	7.0	865	2	US-08-467-602-322	Sequence 322, App
695	113.5	7.1	386	2	US-08-411-295F-207	Sequence 207, App	768	112.5	7.0	865	2	US-08-411-295F-248	Sequence 248, App
696	113.5	7.1	417	2	US-09-949-016-6729	Sequence 6729, Ap	769	112.5	7.0	899	2	US-08-467-602-364	Sequence 364, App
697	113.5	7.1	456	2	US-09-949-016-7564	Sequence 7564, Ap	770	112.5	7.0	899	2	US-08-411-295F-290	Sequence 290, App
698	113.5	7.1	602	1	US-08-168-091A-2	Sequence 2, Appli	771	112.5	7.0	1209	2	US-09-130-158A-2	Sequence 2, Appli
699	113.5	7.1	603	2	US-08-467-602-279	Sequence 279, App	772	112	7.0	281	2	US-10-027-736A-67	Sequence 67, Appl
700	113.5	7.1	603	2	US-08-411-295F-205	Sequence 205, App	773	112	7.0	281	2	US-10-198-053-624	Sequence 624, App
701	113.5	7.1	605	1	US-08-752-307B-8	Sequence 8, Appli	774	112	7.0	354	2	US-10-104-047-2965	Sequence 2965, Ap
702	113.5	7.1	605	2	US-09-707-802-8	Sequence 8, Appli	775	112	7.0	409	2	US-08-467-602-284	Sequence 284, App
703	113.5	7.1	605	2	US-09-391-326-8	Sequence 8, Appli	776	112	7.0	409	2	US-08-411-295F-210	Sequence 210, App
704	113.5	7.1	640	2	US-09-949-016-7565	Sequence 7565, Ap	777	112	7.0	503	2	US-08-999-689A-6	Sequence 6, Appli
705	113.5	7.1	643	4	PCT-US93-00031-19	Sequence 19, Appl	778	112	7.0	503	2	US-09-944-807-4	Sequence 4, Appli
706	113.5	7.1	644	2	PCT-US93-00031-21	Sequence 21, Appl	779	112	7.0	524	2	US-09-270-767-44009	Sequence 44009, A
707	113.5	7.1	647	2	US-09-009-490A-91	Sequence 91, Appl	780	112	7.0	524	2	US-08-467-602-285	Sequence 285, App
708	113.5	7.1	647	2	US-08-482-073-5	Sequence 5, Appli	781	112	7.0	626	2	US-08-411-295F-211	Sequence 211, App
709	113.5	7.1	647	2	US-09-382-262C-92	Sequence 92, Appl	782	112	7.0	626	2	US-08-467-602-283	Sequence 283, App
710	113.5	7.1	647	4	PCT-US93-00031-11	Sequence 11, Appl	783	112	7.0	673	2	US-08-411-295F-209	Sequence 209, App
711	113.5	7.1	647	4	PCT-US93-00031-23	Sequence 23, Appl	784	111	6.9	96	2	US-09-513-999C-7124	Sequence 7124, App
712	113.5	7.1	650	2	US-08-467-602-280	Sequence 280, App	785	111	6.9	375	2	US-08-467-602-242	Sequence 242, App
713	113.5	7.1	650	2	US-08-411-295F-206	Sequence 206, App	786	111	6.9	375	2	US-08-411-295F-168	Sequence 168, App
714	113.5	7.1	729	1	US-08-070-165B-6	Sequence 6, Appli	787	111	6.9	592	2	US-08-467-602-243	Sequence 243, App
715	113.5	7.1	729	1	US-08-885-418-6	Sequence 6, Appli	788	111	6.9	592	2	US-08-411-295F-169	Sequence 169, App
716	113	7.0	352	2	US-09-999-833A-612	Sequence 612, App	789	111	6.9	624	2	US-08-467-602-326	Sequence 326, App
717	113	7.0	352	2	US-10-020-445A-612	Sequence 612, App	790	111	6.9	624	2	US-08-411-295F-252	Sequence 252, App
718	113	7.0	489	2	US-09-667-135-30	Sequence 30, Appl	791	111	6.9	639	2	US-08-467-602-241	Sequence 241, App
719	113	7.0	626	2	US-09-949-016-6213	Sequence 6213, Ap	792	111	6.9	639	2	US-08-411-295F-167	Sequence 167, App
720	113	7.0	664	2	US-09-949-016-7850	Sequence 7850, Ap	793	111	6.9	658	2	US-08-467-602-368	Sequence 368, App
721	112.5	7.0	288	6	5169835-15	Patent No. 5169835	794	111	6.9	658	2	US-08-411-295F-294	Sequence 294, App
722	112.5	7.0	288	1	US-08-147-772-2	Sequence 2, Appli	795	111	6.9	841	2	US-08-467-602-327	Sequence 327, App
723	112.5	7.0	288	1	US-08-456-104-6	Sequence 6, Appli	796	111	6.9	841	2	US-08-411-295F-253	Sequence 253, App
724	112.5	7.0	288	1	US-08-101-624-23	Sequence 23, Appl	797	111	6.9	875	2	US-08-467-602-369	Sequence 369, App
725	112.5	7.0	288	1	US-08-751-767A-6	Sequence 6, Appli	798	111	6.9	875	2	US-08-411-295F-295	Sequence 295, App
726	112.5	7.0	288	2	US-08-153-262-2	Sequence 2, Appli	799	111	6.9	888	2	US-08-467-602-325	Sequence 325, App
727	112.5	7.0	288	2	US-08-479-744A-29	Sequence 29, Appl	800	111	6.9	888	2	US-08-411-295F-251	Sequence 251, App
728	112.5	7.0	288	2	US-08-280-757B-29	Sequence 29, Appl	801	111	6.9	922	2	US-08-467-602-367	Sequence 367, App
729	112.5	7.0	288	2	US-09-159-135-2	Sequence 2, Appli	802	111	6.9	922	2	US-08-411-295F-293	Sequence 293, App
730	112.5	7.0	288	2	US-08-205-697A-19	Sequence 19, Appl	803	110.5	6.9	170	2	US-09-270-767-43106	Sequence 43106, A
731	112.5	7.0	288	2	US-08-702-525-19	Sequence 19, Appl	804	110.5	6.9	512	2	US-08-999-689A-7	Sequence 7, Appli
732	112.5	7.0	288	2	US-09-450-798-2	Sequence 2, Appli	805	110	6.9	336	2	US-10-027-736A-65	Sequence 65, Appl
733	112.5	7.0	288	2	US-08-403-253A-2	Sequence 2, Appli	806	110	6.9	357	2	US-10-027-736A-9	Sequence 9, Appli
734	112.5	7.0	288	2	US-09-651-200-13	Sequence 13, Appl	807	110	6.9	422	2	US-08-753-007A-9	Sequence 9, Appli
735	112.5	7.0	288	2	US-09-667-135-34	Sequence 34, Appl	808	110	6.9	422	2	US-09-398-496-9	Sequence 9, Appli
736	112.5	7.0	288	2	US-08-435-816A-2	Sequence 2, Appli	809	110	6.9	1461	2	US-09-976-594-531	Sequence 531, App
737	112.5	7.0	288	2	US-09-425-762-29	Sequence 29, Appl	810	110	6.9	1503	2	US-09-677-046A-6	Sequence 6, Appli
738	112.5	7.0	288	2	US-09-837-867A-19	Sequence 19, Appl	811	109.5	6.8	316	2	US-09-999-833A-137	Sequence 137, App
739	112.5	7.0	288	2	US-09-310-174B-5	Sequence 5, Appli	812	109.5	6.8	316	2	US-10-020-445A-137	Sequence 137, App
740	112.5	7.0	288	2	US-08-620-461-5	Sequence 5, Appli	813	109.5	6.8	350	2	US-09-651-200-25	Sequence 25, Appl
741	112.5	7.0	288	2	US-08-453-386A-2	Sequence 2, Appli	814	109.5	6.8	350	2	US-09-910-174B-17	Sequence 17, Appl
742	112.5	7.0	288	2	US-09-206-132-6	Sequence 6, Appli	815	109.5	6.8	350	2	US-09-620-461-17	Sequence 17, Appl
743	112.5	7.0	288	2	US-09-425-516-29	Sequence 29, Appl	816	109.5	6.8	373	2	US-09-823-038A-60	Sequence 60, Appl
744	112.5	7.0	288	2	US-09-350-202-2	Sequence 2, Appli	817	109.5	6.8	418	2	US-08-467-602-293	Sequence 293, App
745	112.5	7.0	288	2	US-09-315-789A-15	Sequence 15, Appl	818	109.5	6.8	418	2	US-08-411-295F-219	Sequence 219, App
746	112.5	7.0	288	2	US-08-592-711-2	Sequence 2, Appli	819	109.5	6.8	466	2	US-10-012-231A-267	Sequence 267, App
747	112.5	7.0	288	2	US-09-349-915B-2	Sequence 2, Appli	820	109.5	6.8	466	2	US-10-015-389A-267	Sequence 267, App
748	112.5	7.0	288	4	PCT-US95-02576-19	GENERAL INFORMA	821	109.5	6.8	466	2	US-10-006-768A-267	Sequence 267, App
749	112.5	7.0	352	2	US-08-467-602-239	Sequence 239, App	822	109.5	6.8	466	2	US-10-015-671A-267	Sequence 267, App
750	112.5	7.0	352	2	US-08-411-295F-155	Sequence 155, App	823	109.5	6.8	466	2	US-10-015-393A-267	Sequence 267, App
751	112.5	7.0	569	2	US-08-467-602-237	Sequence 237, App	824	109.5	6.8	466	2	US-10-011-833A-267	Sequence 267, App
752	112.5	7.0	601	2	US-08-411-295F-163	Sequence 163, App	825	109.5	6.8	466	2	US-10-006-041A-267	Sequence 267, App
753	112.5	7.0	601	2	US-08-470-335-233	Sequence 233, App	826	109.5	6.8	466	2	US-10-012-064A-267	Sequence 267, App
754	112.5	7.0	601	2	US-08-467-602-323	Sequence 323, App	827	109.5	6.8	529	2	US-09-383-586-31	Sequence 31, Appl
755	112.5	7.0	601	2	US-08-411-295F-249	Sequence 249, App	828	109.5	6.8	529	2	US-09-823-038A-31	Sequence 31, Appl
756	112.5	7.0	616	2	US-08-467-602-238	Sequence 238, App	829	109.5	6.8	534	2	US-09-651-200-6	Sequence 6, Appli
757	112.5	7.0	616	2	US-08-411-295F-164	Sequence 164, App	830	109.5	6.8	534	2	US-09-651-200-24	Sequence 24, Appl

831	109.5	6.8	635	2	US-08-467-602-294	Sequence 294, App	904	108.5	6.8	897	2	US-08-411-295F-263	Sequence 263, App
832	109.5	6.8	635	2	US-08-411-295F-220	Sequence 220, App	905	108.5	6.8	924	1	US-08-481-130-28	Sequence 28, Appl
833	109.5	6.8	682	2	US-08-467-602-295	Sequence 295, App	906	108.5	6.8	924	1	US-08-481-130-28	Sequence 28, Appl
834	109.5	6.8	682	2	US-08-411-295F-221	Sequence 221, App	907	108.5	6.8	924	1	US-08-481-130-28	Sequence 28, Appl
835	109.5	6.8	79	2	US-09-621-767-4730	Sequence 4730, App	908	108.5	6.8	924	1	US-08-481-130-28	Sequence 28, Appl
836	109.5	6.8	286	2	US-09-270-767-44618	Sequence 44618, A	909	108.5	6.8	931	2	US-08-467-602-379	Sequence 379, App
837	109.5	6.8	395	2	US-08-467-602-290	Sequence 290, App	910	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
838	109.5	6.8	395	2	US-08-411-295F-216	Sequence 216, App	911	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
839	109.5	6.8	405	2	US-08-755-235-4	Sequence 4, Appli	912	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
840	109.5	6.8	612	2	US-08-467-602-291	Sequence 291, App	913	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
841	109.5	6.8	612	2	US-08-411-295F-217	Sequence 217, App	914	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
842	109.5	6.8	619	2	US-10-104-047-2048	Sequence 2048, App	915	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
843	109.5	6.8	630	1	US-08-752-307B-14	Sequence 14, Appl	916	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
844	109.5	6.8	630	2	US-09-707-802-14	Sequence 14, Appl	917	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
845	109.5	6.8	630	2	US-09-991-326-14	Sequence 14, Appl	918	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
846	109.5	6.8	659	2	US-08-467-602-292	Sequence 292, App	919	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
847	109.5	6.8	659	2	US-08-411-295F-218	Sequence 218, App	920	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
848	109.5	6.8	816	2	US-09-949-016-10904	Sequence 10904, A	921	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
849	109.5	6.8	885	2	US-10-104-047-2946	Sequence 2946, App	922	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
850	109.5	6.8	917	1	US-08-245-295-2	Sequence 2, Appli	923	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
851	109.5	6.8	917	1	US-08-481-130-2	Sequence 2, Appli	924	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
852	109.5	6.8	917	1	US-08-556-984A-2	Sequence 2, Appli	925	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
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854	109.5	6.8	917	1	US-08-487-595-2	Sequence 2, Appli	927	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
855	109.5	6.8	1474	2	US-09-677-046A-4	Sequence 4, Appli	928	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
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889	108.5	6.8	637	1	US-07-847-743B-28	Sequence 28, Appl	962	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
890	108.5	6.8	637	1	US-08-456-201-28	Sequence 28, Appl	963	108.5	6.8	931	2	US-08-411-295F-305	Sequence 305, App
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903	108.5	6.8	897	2	US-08-467-602-337	Sequence 337, App	976	108.5	6.8	931	2	US-08-467-602-375	Sequence 375, App

977	108	6.7	861	2	US-08-411-295F-238	Sequence 238, App	1050	107.5	6.7	647	2	US-08-411-295F-297	Sequence 297, App
978	108	6.7	861	2	US-08-411-295F-301	Sequence 301, App	1051	107.5	6.7	684	2	US-08-467-602-259	Sequence 259, App
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981	108	6.7	864	2	US-08-411-295F-235	Sequence 235, App	1054	107.5	6.7	733	1	US-07-921-807B-6	Sequence 6, Appl1
982	108	6.7	874	2	US-08-470-335-238	Sequence 238, App	1055	107.5	6.7	733	1	US-08-441-944A-6	Sequence 6, Appl1
983	108	6.7	874	2	US-08-467-602-334	Sequence 334, App	1056	107.5	6.7	733	2	US-08-439-992A-4	Sequence 4, Appl1
984	108	6.7	874	2	US-08-411-295F-260	Sequence 260, App	1057	107.5	6.7	733	2	US-09-620-561-4	Sequence 4, Appl1
985	108	6.7	875	2	US-08-467-602-306	Sequence 306, App	1058	107.5	6.7	830	2	US-08-470-335-231	Sequence 231, App
986	108	6.7	875	2	US-08-411-295F-232	Sequence 232, App	1059	107.5	6.7	830	2	US-08-467-602-330	Sequence 330, App
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989	108	6.7	886	2	US-08-467-602-342	Sequence 342, App	1062	107.5	6.7	864	2	US-08-411-295F-298	Sequence 298, App
990	108	6.7	886	2	US-08-411-295F-268	Sequence 268, App	1063	107.5	6.7	877	2	US-08-470-335-232	Sequence 232, App
991	108	6.7	889	2	US-08-467-602-340	Sequence 340, App	1064	107.5	6.7	877	2	US-08-467-602-331	Sequence 331, App
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996	108	6.7	898	2	US-08-411-295F-277	Sequence 277, App	1069	107	6.7	110	2	US-09-513-999C-7253	Sequence 7253, Ap
997	108	6.7	899	2	US-08-470-335-249	Sequence 249, App	1070	107	6.7	389	2	US-08-467-602-276	Sequence 276, App
998	108	6.7	899	2	US-08-467-602-301	Sequence 301, App	1071	107	6.7	389	2	US-08-411-295F-202	Sequence 202, App
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1000	108	6.7	902	2	US-08-470-335-242	Sequence 242, App	1073	107	6.7	488	2	US-09-499-846-12	Sequence 12, Appl
1001	108	6.7	902	2	US-08-467-602-296	Sequence 296, App	1074	107	6.7	497	2	US-09-499-846-6	Sequence 6, Appl1
1002	108	6.7	902	2	US-08-411-295F-222	Sequence 222, App	1075	107	6.7	497	2	US-09-499-846-10	Sequence 10, Appl
1003	108	6.7	908	2	US-08-470-335-252	Sequence 252, App	1076	107	6.7	525	2	US-09-499-846-4	Sequence 4, Appl1
1004	108	6.7	908	2	US-08-467-602-313	Sequence 313, App	1077	107	6.7	525	2	US-09-499-846-8	Sequence 8, Appl1
1005	108	6.7	908	2	US-08-467-602-376	Sequence 376, App	1078	107	6.7	606	2	US-08-467-602-277	Sequence 277, App
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1007	108	6.7	908	2	US-08-411-295F-302	Sequence 302, App	1080	107	6.7	653	2	US-08-467-602-275	Sequence 275, App
1008	108	6.7	909	2	US-08-467-602-348	Sequence 348, App	1081	107	6.7	653	2	US-08-411-295F-201	Sequence 201, App
1009	108	6.7	909	2	US-08-411-295F-274	Sequence 274, App	1082	106.5	6.6	210	2	US-09-451-291-10	Sequence 10, Appl
1010	108	6.7	911	2	US-08-470-335-245	Sequence 245, App	1083	106.5	6.6	316	2	US-09-915-789A-3	Sequence 3, Appl1
1011	108	6.7	911	2	US-08-467-602-310	Sequence 310, App	1084	106.5	6.6	386	2	US-08-467-602-218	Sequence 218, App
1012	108	6.7	911	2	US-08-411-295F-236	Sequence 236, App	1085	106.5	6.6	386	2	US-08-411-295F-144	Sequence 144, App
1013	108	6.7	918	2	US-08-467-602-357	Sequence 357, App	1086	106.5	6.6	603	2	US-08-467-602-216	Sequence 216, App
1014	108	6.7	918	2	US-08-411-295F-283	Sequence 283, App	1087	106.5	6.6	603	2	US-08-411-295F-142	Sequence 142, App
1015	108	6.7	922	2	US-08-467-602-304	Sequence 304, App	1088	106.5	6.6	650	2	US-08-467-602-217	Sequence 217, App
1016	108	6.7	922	2	US-08-411-295F-230	Sequence 230, App	1089	106.5	6.6	650	2	US-08-411-295F-143	Sequence 143, App
1017	108	6.7	931	2	US-08-467-602-316	Sequence 316, App	1090	106.5	6.6	731	1	US-08-070-165F-10	Sequence 10, Appl
1018	108	6.7	931	2	US-08-411-295F-242	Sequence 242, App	1091	106.5	6.6	731	1	US-08-885-418-10	Sequence 10, Appl
1019	108	6.7	933	2	US-08-467-602-343	Sequence 343, App	1092	106.5	6.6	879	1	US-08-554-612C-1	Sequence 1, Appl1
1020	108	6.7	933	2	US-08-411-295F-269	Sequence 269, App	1093	106	6.6	355	2	US-08-467-602-234	Sequence 234, App
1021	108	6.7	936	2	US-08-467-602-338	Sequence 338, App	1094	106	6.6	355	2	US-08-411-295F-160	Sequence 160, App
1022	108	6.7	936	2	US-08-411-295F-264	Sequence 264, App	1095	106	6.6	443	2	US-08-467-603-263	Sequence 263, App
1023	108	6.7	942	2	US-08-467-602-355	Sequence 355, App	1096	106	6.6	443	2	US-08-411-295F-189	Sequence 189, App
1024	108	6.7	942	2	US-08-411-295F-281	Sequence 281, App	1097	106	6.6	572	2	US-08-467-602-235	Sequence 235, App
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1028	108	6.7	956	2	US-08-411-295F-272	Sequence 272, App	1101	106	6.6	604	2	US-08-411-295F-244	Sequence 244, App
1029	108	6.7	965	2	US-08-467-602-358	Sequence 358, App	1102	106	6.6	619	2	US-08-467-602-233	Sequence 233, App
1030	108	6.7	965	2	US-08-411-295F-284	Sequence 284, App	1103	106	6.6	619	2	US-08-411-295F-159	Sequence 159, App
1031	107.5	6.7	262	2	US-10-104-047-3119	Sequence 3119, Ap	1104	106	6.6	638	2	US-08-467-602-360	Sequence 360, App
1032	107.5	6.7	316	2	US-09-910-174B-24	Sequence 24, Appl	1105	106	6.6	638	2	US-08-411-295F-286	Sequence 286, App
1033	107.5	6.7	316	2	US-09-620-461-24	Sequence 24, Appl	1106	106	6.6	660	2	US-08-467-603-264	Sequence 264, App
1034	107.5	6.7	316	2	US-09-915-789A-1	Sequence 1, Appl1	1107	106	6.6	760	2	US-08-467-602-262	Sequence 262, App
1035	107.5	6.7	358	2	US-09-719-243-3	Sequence 3, Appl1	1108	106	6.6	760	2	US-08-411-295F-190	Sequence 190, App
1036	107.5	6.7	364	2	US-08-467-602-245	Sequence 245, App	1109	106	6.6	707	2	US-08-411-295F-188	Sequence 188, App
1037	107.5	6.7	364	2	US-08-411-295F-171	Sequence 171, App	1110	106	6.6	821	2	US-08-470-335-228	Sequence 228, App
1038	107.5	6.7	420	2	US-08-467-602-260	Sequence 260, App	1111	106	6.6	821	2	US-08-467-602-319	Sequence 319, App
1039	107.5	6.7	420	2	US-08-411-295F-186	Sequence 186, App	1112	106	6.6	821	2	US-08-411-295F-245	Sequence 245, App
1040	107.5	6.7	581	2	US-08-467-602-246	Sequence 246, App	1113	106	6.6	855	2	US-08-467-603-361	Sequence 361, App
1041	107.5	6.7	591	2	US-08-411-295F-172	Sequence 172, App	1114	106	6.6	855	2	US-08-411-295F-287	Sequence 287, App
1042	107.5	6.7	613	2	US-08-470-335-230	Sequence 230, App	1115	106	6.6	868	2	US-08-470-335-229	Sequence 229, App
1043	107.5	6.7	613	2	US-08-467-602-329	Sequence 329, App	1116	106	6.6	868	2	US-08-467-602-317	Sequence 317, App
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1047	107.5	6.7	637	2	US-08-467-602-258	Sequence 258, App	1120	105.5	6.6	235	2	US-09-646-561-12	Sequence 12, Appl
1048	107.5	6.7	637	2	US-08-411-295F-184	Sequence 184, App	1121	105.5	6.6	267	2	US-09-345-468-19	Sequence 19, Appl
1049	107.5	6.7	647	2	US-08-467-602-371	Sequence 371, App	1122	105.5	6.6	267	2	US-09-414-453A-19	Sequence 19, Appl

1123	105.5	6.6	292	2	US-09-345-468-18	Sequence 18, Appl	1196	103	6.4	240	1	US-08-471-570-12	Sequence 12, Appl
1124	105.5	6.6	292	2	US-09-414-453A-18	Sequence 18, Appl	1197	103	6.4	428	2	US-09-949-016-6625	Sequence 6625, Ap
1125	105.5	6.6	313	2	US-09-345-468-16	Sequence 16, Appl	1198	103	6.4	429	2	US-08-467-602-269	Sequence 269, App
1126	105.5	6.6	313	2	US-09-414-453A-16	Sequence 16, Appl	1199	103	6.4	429	2	US-08-411-295F-195	Sequence 195, App
1127	105.5	6.6	498	2	US-09-354-551-2	Sequence 2, Appli	1200	103	6.4	433	2	US-09-949-016-8521	Sequence 8521, Ap
1128	105.5	6.6	624	1	US-08-642-406A-22	Sequence 22, Appl	1201	103	6.4	473	2	US-09-171-1945-131	Sequence 131, App
1129	105.5	6.6	624	2	US-09-199-534-22	Sequence 22, Appl	1202	103	6.4	473	2	US-09-910-059-131	Sequence 131, App
1130	105.5	6.6	624	2	US-09-199-534-22	Sequence 22, Appl	1203	103	6.4	473	2	US-08-467-602-270	Sequence 270, App
1131	105.5	6.6	624	2	US-09-491-322-22	Sequence 22, Appl	1204	103	6.4	646	2	US-08-411-295F-196	Sequence 196, App
1132	105.5	6.6	645	1	US-07-847-743B-27	Sequence 27, Appl	1205	103	6.4	693	2	US-08-467-602-271	Sequence 271, App
1133	105.5	6.6	645	1	US-08-456-201-27	Sequence 27, Appl	1206	103	6.4	693	2	US-08-411-295F-197	Sequence 197, App
1134	105.5	6.6	645	1	US-08-428-326-4	Sequence 4, Appli	1207	103	6.4	1140	2	US-09-579-692B-8	Sequence 8, Appli
1135	105.5	6.6	645	1	US-08-428-927-4	Sequence 4, Appli	1208	102.5	6.4	257	2	US-09-489-039A-13452	Sequence 13452, A
1136	105.5	6.6	645	1	US-08-428-398-4	Sequence 4, Appli	1209	102.5	6.4	261	2	US-09-245-764-7	Sequence 7, Appli
1137	105.5	6.6	645	1	US-08-339-517-4	Sequence 4, Appli	1210	102.5	6.4	263	2	US-08-411-295F-4	Sequence 4, Appli
1138	105.5	6.6	645	1	US-08-456-241-27	Sequence 27, Appl	1211	102.5	6.4	418	2	US-08-467-602-230	Sequence 230, App
1139	105.5	6.6	645	2	US-09-020-880-93	Sequence 93, Appl	1212	102.5	6.4	418	2	US-08-411-295F-156	Sequence 156, App
1140	105.5	6.6	645	2	US-09-101-544-93	Sequence 93, Appl	1213	102.5	6.4	432	2	US-08-467-602-266	Sequence 266, App
1141	105.5	6.6	645	2	US-09-037-681-3	Sequence 3, Appli	1214	102.5	6.4	432	2	US-08-411-295F-192	Sequence 192, App
1142	105.5	6.6	645	4	PCT-US92-04295A-27	Sequence 27, Appl	1215	102.5	6.4	584	2	US-09-910-174B-16	Sequence 16, Appl
1143	105.5	6.6	732	1	US-07-847-743B-9	Sequence 9, Appli	1216	102.5	6.4	584	2	US-09-620-461-16	Sequence 16, Appl
1144	105.5	6.6	732	1	US-08-456-201-9	Sequence 9, Appli	1217	102.5	6.4	610	1	US-08-724-394B-5	Sequence 5, Appli
1145	105.5	6.6	732	1	US-08-456-241-9	Sequence 9, Appli	1218	102.5	6.4	635	2	US-08-467-602-231	Sequence 231, App
1146	105.5	6.6	732	4	PCT-US92-04295A-9	Sequence 9, Appli	1219	102.5	6.4	635	2	US-08-411-295F-157	Sequence 157, App
1147	105.5	6.6	703	2	US-08-434-000A-2	Sequence 2, Appli	1220	102.5	6.4	649	2	US-08-467-602-267	Sequence 267, App
1148	105.5	6.6	773	2	US-09-312-157-2	Sequence 2, Appli	1221	102.5	6.4	649	2	US-08-411-295F-193	Sequence 193, App
1149	105.5	6.6	773	2	US-09-717-888-2	Sequence 2, Appli	1222	102.5	6.4	668	2	US-09-173-151A-35	Sequence 35, Appl
1150	105.5	6.6	773	2	US-09-818-247-6	Sequence 6, Appli	1223	102.5	6.4	682	2	US-08-467-602-232	Sequence 232, App
1151	105	6.5	144	6	5169835-8	Patent No. 5169835	1224	102.5	6.4	682	2	US-08-411-295F-158	Sequence 158, App
1152	105	6.5	374	2	US-10-027-736A-10	Sequence 10, Appl	1225	102.5	6.4	682	2	US-08-411-295F-159	Sequence 258, App
1153	105	6.5	409	2	US-08-467-602-221	Sequence 221, App	1226	102.5	6.4	696	2	US-08-467-602-268	Sequence 194, App
1154	105	6.5	409	2	US-08-411-295F-147	Sequence 147, App	1227	102	6.4	63	2	US-09-621-976-6056	Sequence 6056, Ap
1155	105	6.5	626	2	US-08-467-602-222	Sequence 222, App	1228	102	6.4	395	2	US-08-467-602-227	Sequence 227, App
1156	105	6.5	626	2	US-08-411-295F-148	Sequence 148, App	1229	102	6.4	395	2	US-08-411-295F-153	Sequence 153, App
1157	105	6.5	673	2	US-08-467-602-220	Sequence 220, App	1230	102	6.4	416	2	US-09-638-649-1	Sequence 1, Appli
1158	105	6.5	673	2	US-08-411-295F-146	Sequence 146, App	1231	102	6.4	416	2	US-08-755-235-2	Sequence 2, Appli
1159	104.5	6.5	259	2	US-10-104-047-2303	Sequence 2303, Ap	1232	102	6.4	416	2	US-09-638-648-1	Sequence 1, Appli
1160	104.5	6.5	518	2	US-09-919-172-20	Sequence 20, Appl	1233	102	6.4	612	2	US-08-467-602-228	Sequence 228, App
1161	104.5	6.5	645	2	US-08-753-007A-10	Sequence 10, Appl	1234	102	6.4	612	2	US-08-411-295F-154	Sequence 154, App
1162	104.5	6.5	645	2	US-09-338-496-10	Sequence 10, Appl	1235	102	6.4	659	2	US-08-467-602-229	Sequence 229, App
1163	104.5	6.5	777	1	US-08-874-678-3	Sequence 3, Appli	1236	102	6.4	659	2	US-08-411-295F-155	Sequence 155, App
1164	104.5	6.5	777	2	US-08-643-839-3	Sequence 3, Appli	1237	101.5	6.3	318	1	US-08-633-148-4	Sequence 4, Appli
1165	104.5	6.5	777	2	US-09-348-886-3	Sequence 3, Appli	1238	101.5	6.3	323	2	US-09-684-708A-25	Sequence 25, Appl
1166	104.5	6.5	777	2	US-10-105-901A-3	Sequence 3, Appli	1239	101.5	6.3	332	2	US-09-062-365-1	Sequence 1, Appli
1167	104	6.5	236	2	US-09-015-734-7	Sequence 7, Appli	1240	101.5	6.3	339	2	US-09-799-152-2	Sequence 2, Appli
1168	104	6.5	236	2	US-09-515-311-7	Sequence 7, Appli	1241	101.5	6.3	340	1	US-08-633-148-2	Sequence 2, Appli
1169	104	6.5	236	2	US-10-434-817-7	Sequence 7, Appli	1242	101.5	6.3	345	1	US-08-332-562A-132	Sequence 132, App
1170	104	6.5	255	2	US-09-015-734-2	Sequence 2, Appli	1243	101.5	6.3	398	2	US-08-467-602-224	Sequence 224, App
1171	104	6.5	255	2	US-09-515-311-2	Sequence 2, Appli	1244	101.5	6.3	398	2	US-08-411-295F-150	Sequence 150, App
1172	104	6.5	255	2	US-10-434-817-2	Sequence 2, Appli	1245	101.5	6.3	615	2	US-08-467-602-225	Sequence 225, App
1173	104	6.5	802	2	US-09-173-151A-33	Sequence 33, Appli	1246	101.5	6.3	615	2	US-08-411-295F-151	Sequence 151, App
1174	103.5	6.4	388	1	US-08-429-742-4	Sequence 4, Appli	1247	101.5	6.3	662	2	US-08-467-602-226	Sequence 226, App
1175	103.5	6.4	452	2	US-08-467-602-272	Sequence 272, App	1248	101.5	6.3	662	2	US-08-411-295F-152	Sequence 152, App
1176	103.5	6.4	452	2	US-08-411-295F-198	Sequence 198, App	1249	101	6.3	205	2	US-09-451-291-11	Sequence 11, Appl
1177	103.5	6.4	669	2	US-08-467-602-273	Sequence 273, App	1250	101	6.3	280	2	US-09-270-767-43068	Sequence 43068, A
1178	103.5	6.4	669	2	US-08-411-295F-199	Sequence 199, App	1251	101	6.3	423	2	US-08-467-602-255	Sequence 255, App
1179	103.5	6.4	716	2	US-08-467-602-274	Sequence 274, App	1252	101	6.3	423	2	US-08-411-295F-181	Sequence 181, App
1180	103.5	6.4	731	1	US-08-411-295F-200	Sequence 200, App	1253	101	6.3	625	1	US-07-847-743B-26	Sequence 26, Appl
1181	103.5	6.4	731	1	US-07-921-807B-5	Sequence 5, Appli	1254	101	6.3	625	1	US-08-456-201-26	Sequence 26, Appl
1182	103.5	6.4	731	1	US-08-441-944A-5	Sequence 5, Appli	1255	101	6.3	625	1	PCT-US92-04295A-26	Sequence 26, Appl
1183	103.5	6.4	731	2	US-08-439-992A-3	Sequence 3, Appli	1256	101	6.3	625	4	US-08-467-602-256	Sequence 256, App
1184	103.5	6.4	731	2	US-09-620-561-3	Sequence 3, Appli	1257	101	6.3	640	2	US-08-411-295F-182	Sequence 182, App
1185	103	6.4	58	2	US-09-621-976-5931	Sequence 5931, Ap	1258	101	6.3	640	2	US-07-847-743B-8	Sequence 8, Appli
1186	103	6.4	58	2	US-09-621-976-5963	Sequence 5963, Ap	1259	101	6.3	669	1	US-08-456-201-13	Sequence 13, Appl
1187	103	6.4	58	2	US-09-621-976-6579	Sequence 6579, Ap	1260	101	6.3	669	1	US-08-456-201-11	Sequence 11, Appl
1188	103	6.4	71	2	US-09-621-976-5970	Sequence 5970, Ap	1261	101	6.3	669	1	US-08-330-161-11	Sequence 11, Appl
1189	103	6.4	71	2	US-09-621-976-6815	Sequence 6815, Ap	1262	101	6.3	669	1	US-08-456-241-8	Sequence 8, Appli
1190	103	6.4	71	2	US-09-621-976-6875	Sequence 6875, Ap	1263	101	6.3	669	1	US-08-456-241-13	Sequence 13, Appl
1191	103	6.4	133	2	US-10-104-047-3128	Sequence 3128, Ap	1264	101	6.3	669	1	US-08-440-401-11	Sequence 11, Appl
1192	103	6.4	208	2	US-09-460-384-36	Sequence 36, Appl	1265	101	6.3	669	1	US-08-419-878B-11	Sequence 11, Appl
1193	103	6.4	216	2	US-09-666-267B-8	Sequence 8, Appli	1266	101	6.3	669	1	US-09-173-480-11	Sequence 11, Appl
1194	103	6.4	216	2	US-09-454-651B-23	Sequence 23, Appl	1267	101	6.3	669	1		
1195	103	6.4	226	2	US-09-915-789A-21	Sequence 21, Appl	1268	101	6.3	669	2		

1269	101	6.3	669	2	US-10-022-609-11	Sequence 11, Appl	1342	99	6.2	273	2	US-09-270-767-32843	Sequence 32843, A
1270	101	6.3	669	4	PCT-US92-04298A-8	Sequence 8, Appli	1343	99	6.2	273	2	US-09-270-767-48060	Sequence 48060, A
1271	101	6.3	669	4	PCT-US92-04298A-13	Sequence 13, Appl	1344	99	6.2	431	2	US-09-592-998C-9	Sequence 9, Appli
1272	101	6.3	687	2	US-08-467-602-254	Sequence 254, App	1345	99	6.2	435	2	US-09-592-998C-10	Sequence 10, Appl
1273	101	6.3	687	2	US-08-411-295F-180	Sequence 180, App	1346	99	6.2	466	1	US-08-432-016-4	Sequence 4, Appli
1274	100.5	6.3	95	2	US-08-928-383B-17	Sequence 17, Appl	1347	99	6.2	466	1	US-08-684-594-4	Sequence 4, Appli
1275	100.5	6.3	210	2	US-08-467-602-278	Sequence 278, App	1348	99	6.2	898	1	US-08-808-983-5	Sequence 5, Appli
1276	100.5	6.3	210	2	US-08-411-295F-204	Sequence 204, App	1349	99	6.2	898	1	US-09-306-902A-5	Sequence 5, Appli
1277	100.5	6.3	230	2	US-09-910-174B-32	Sequence 32, Appl	1350	98.5	6.1	280	2	US-09-341-018-56	Sequence 56, Appl
1278	100.5	6.3	230	2	US-09-451-291-3	Sequence 3, Appli	1351	98.5	6.1	280	2	US-08-470-335-192	Sequence 192, App
1279	100.5	6.3	230	2	US-09-645-069-23	Sequence 23, Appl	1352	98.5	6.1	280	2	US-08-470-339-192	Sequence 192, App
1280	100.5	6.3	230	2	US-09-644-934-11	Sequence 11, Appl	1353	98.5	6.1	280	2	US-08-467-602-386	Sequence 386, App
1281	100.5	6.3	342	2	US-09-684-708A-27	Sequence 27, Appl	1354	98.5	6.1	280	2	US-08-411-295F-49	Sequence 49, App
1282	100	6.2	112	2	US-09-858-664B-24	Sequence 24, Appl	1355	98.5	6.1	280	2	US-08-411-295F-95	Sequence 95, App
1283	100	6.2	112	2	US-10-274-978-25	Sequence 25, Appl	1356	98.5	6.1	319	2	US-09-910-174B-12	Sequence 12, App
1284	100	6.2	112	2	US-10-697-263-25	Sequence 25, Appl	1357	98.5	6.1	319	2	US-09-620-461-12	Sequence 12, App
1285	100	6.2	194	2	US-09-949-016-8618	Sequence 8618, Ap	1358	98.5	6.1	342	1	US-08-724-394A-6	Sequence 6, Appli
1286	100	6.2	201	2	US-09-015-734-12	Sequence 12, Appl	1359	98.5	6.1	349	2	US-08-470-335-188	Sequence 188, App
1287	100	6.2	201	2	US-09-515-311-12	Sequence 12, Appl	1360	98.5	6.1	357	2	US-09-910-174B-14	Sequence 14, Appl
1288	100	6.2	201	2	US-10-434-817-12	Sequence 12, Appl	1361	98.5	6.1	357	2	US-09-620-461-14	Sequence 14, Appl
1289	100	6.2	282	2	US-09-461-912A-38	Sequence 38, Appl	1362	98.5	6.1	382	2	US-08-467-602-382	Sequence 382, App
1290	100	6.2	389	2	US-08-467-602-213	Sequence 38, Appl	1363	98.5	6.1	411	2	US-08-470-339-189	Sequence 189, App
1291	100	6.2	389	2	US-08-411-295F-139	Sequence 139, App	1364	98.5	6.1	414	2	US-08-470-339-188	Sequence 188, App
1292	100	6.2	536	2	US-09-910-174B-9	Sequence 9, Appli	1365	98.5	6.1	422	1	US-08-036-555B-170	Sequence 170, App
1293	100	6.2	536	2	US-09-620-461-9	Sequence 9, Appli	1366	98.5	6.1	422	1	US-08-469-569-170	Sequence 170, App
1294	100	6.2	536	2	US-09-949-016-6122	Sequence 6122, Ap	1367	98.5	6.1	422	1	US-08-428-926-3	Sequence 3, Appli
1295	100	6.2	540	2	US-09-949-016-11644	Sequence 11644, A	1368	98.5	6.1	422	1	US-08-249-322A-170	Sequence 170, App
1296	100	6.2	606	2	US-08-467-602-214	Sequence 214, App	1369	98.5	6.1	422	1	US-08-428-927-3	Sequence 3, Appli
1297	100	6.2	606	2	US-08-411-295F-140	Sequence 140, App	1370	98.5	6.1	422	1	US-08-428-298-3	Sequence 3, Appli
1298	100	6.2	653	2	US-08-467-602-212	Sequence 212, App	1371	98.5	6.1	422	1	US-08-339-517-3	Sequence 3, Appli
1299	100	6.2	653	2	US-08-411-295F-138	Sequence 138, App	1372	98.5	6.1	422	1	US-08-469-526A-170	Sequence 170, App
1300	99.5	6.2	176	2	US-08-467-602-236	Sequence 236, App	1373	98.5	6.1	422	1	US-08-734-591A-170	Sequence 170, App
1301	99.5	6.2	176	2	US-08-411-295F-162	Sequence 162, App	1374	98.5	6.1	422	1	US-08-469-660-170	Sequence 170, App
1302	99.5	6.2	240	2	US-09-270-767-32134	Sequence 32134, A	1375	98.5	6.1	422	2	US-08-341-018-72	Sequence 72, Appl
1303	99.5	6.2	425	2	US-08-470-335-226	Sequence 226, App	1376	98.5	6.1	422	2	US-08-470-335-170	Sequence 170, App
1304	99.5	6.2	425	2	US-08-467-602-320	Sequence 320, App	1377	98.5	6.1	422	2	US-08-735-021-170	Sequence 170, App
1305	99.5	6.2	425	2	US-08-411-295F-246	Sequence 246, App	1378	98.5	6.1	422	2	US-08-734-664A-170	Sequence 170, App
1306	99.5	6.2	459	2	US-08-467-602-362	Sequence 362, App	1379	98.5	6.1	422	2	US-08-470-339-170	Sequence 170, App
1307	99.5	6.2	459	2	US-08-411-295F-288	Sequence 288, App	1380	98.5	6.1	422	2	US-08-467-602-324	Sequence 324, App
1308	99.5	6.2	612	1	US-08-359-705B-8	Sequence 8, Appli	1381	98.5	6.1	422	2	US-08-411-295F-65	Sequence 65, Appl
1309	99.5	6.2	612	1	US-08-286-846A-8	Sequence 8, Appli	1382	98.5	6.1	422	2	US-08-411-295F-66	Sequence 66, Appl
1310	99.5	6.2	612	1	US-08-457-880A-8	Sequence 8, Appli	1383	98.5	6.1	422	2	US-08-411-295F-69	Sequence 69, Appl
1311	99.5	6.2	612	1	US-08-444-622A-8	Sequence 8, Appli	1384	98.5	6.1	422	2	US-08-411-295F-103	Sequence 103, App
1312	99.5	6.2	612	2	US-08-942-562-8	Sequence 8, Appli	1385	98.5	6.1	422	2	US-08-411-295F-250	Sequence 250, App
1313	99.5	6.2	612	2	US-09-156-923-8	Sequence 8, Appli	1386	98.5	6.1	422	4	PCT-US94-05083C-166	Sequence 166, App
1314	99.5	6.2	612	2	US-09-907-794A-292	Sequence 292, App	1387	98.5	6.1	422	4	PCT-US95-06846A-170	Sequence 185, App
1315	99.5	6.2	640	2	US-09-905-125A-292	Sequence 292, App	1388	98.5	6.1	422	4	US-08-467-602-328	Sequence 170, App
1316	99.5	6.2	640	2	US-09-902-775A-292	Sequence 292, App	1389	98.5	6.1	445	2	US-08-467-602-328	Sequence 328, App
1317	99.5	6.2	640	2	US-09-906-700-292	Sequence 292, App	1390	98.5	6.1	445	2	US-08-411-295F-254	Sequence 254, App
1318	99.5	6.2	640	2	US-09-903-603A-292	Sequence 292, App	1391	98.5	6.1	456	2	US-08-467-602-365	Sequence 366, App
1319	99.5	6.2	640	2	US-09-904-920A-292	Sequence 292, App	1392	98.5	6.1	456	2	US-08-411-295F-282	Sequence 282, App
1320	99.5	6.2	640	2	US-09-909-064-292	Sequence 292, App	1393	98.5	6.1	479	2	US-08-467-602-370	Sequence 370, App
1321	99.5	6.2	640	2	US-09-905-381A-292	Sequence 292, App	1394	98.5	6.1	479	2	US-08-411-295F-236	Sequence 236, App
1322	99.5	6.2	640	2	US-09-906-618-292	Sequence 292, App	1395	98.5	6.1	604	2	US-09-949-016-9548	Sequence 9548, App
1323	99.5	6.2	640	2	US-09-906-646-292	Sequence 292, App	1396	98.5	6.1	551	2	US-09-270-767-44877	Sequence 44877, A
1324	99.5	6.2	640	2	US-09-904-462-292	Sequence 292, App	1397	98.5	6.1	723	1	US-07-640-029-3	Sequence 3, Appli
1325	99.5	6.2	640	2	US-09-901-181-501	Sequence 501, App	1398	98.5	6.1	723	2	US-08-478-208-32	Sequence 32, Appl
1326	99.5	6.2	640	2	US-09-991-444-501	Sequence 501, App	1399	98.5	6.1	738	2	US-09-336-536-73	Sequence 73, Appl
1327	99.5	6.2	640	2	US-09-906-722A-292	Sequence 292, App	1400	98	6.1	140	2	US-08-986-485-4	Sequence 20, Appl
1328	99.5	6.2	640	2	US-09-997-333-501	Sequence 501, App	1401	98	6.1	215	2	US-09-915-789A-20	Sequence 10, Appl
1329	99.5	6.2	640	2	US-09-992-598-501	Sequence 501, App	1402	98	6.1	501	2	US-08-891-845-10	Sequence 10, Appl
1330	99.5	6.2	640	2	US-08-359-705B-6	Sequence 6, Appli	1403	98	6.1	501	2	US-09-514-573-10	Sequence 10, Appl
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ALIGNMENTS

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RESULT 1
US-09-254-465A-9
; Sequence 9, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 9
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-9
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Best Local Similarity 100.0%; Pred. No. 9.1e-149;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      301  KAAAGGSRGQEF 312
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RESULT 2
US-09-907-794A-64
; Sequence 64, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999

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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-907-794A-64

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Best Local Similarity 100.0%; Pred. No. 9.1e-149;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      301  KAAAGGSRGQEF 312
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RESULT 3
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; Sequence 64, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A

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; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-64

Query Match 100.0%; Score 1605; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 9.1e-149;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-902-775A-64

; Sequence 64, Application US/09902775A
; Patent No. 686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsens, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-64

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Db 241 IAAVVVVVALVISVCGLGVCYAQRKGYSKETSFKGNSSSKATMTSENQWLTVPVIALW 300
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RESULT 9

US-09-905-381A-64
; Sequence 64, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-09-08
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; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
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; PRIOR FILING DATE: 2000-01-05
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-381A-64
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; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey


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; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-462-64

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; Sequence 64, Application US/09902736A
; Patent No. 6894148
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
```

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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,736A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-736A-64

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US-09-906-722A-64
; Sequence 64, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Aghkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Pong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C61
; CURRENT FILING DATE: 2001-07-16
; PRIOR FILING DATE: 2000-02-22
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
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; ORGANISM: Homo sapiens
US-09-906-722A-64

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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8	1144	71.3	298	7 US-11-025-834A-14
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21	461.5	28.8	362	6 US-10-821-234-1148
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28	404	25.2	299	7 US-11-000-463-747
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80	161	10.0	344	7	US-11-050-857-959	Sequence 959, App
81	159.5	9.9	961	7	US-11-051-724-42	Sequence 42, Appl
82	158	9.8	842	7	US-11-124-368A-171	Sequence 171, App
83	158	9.8	1343	6	US-10-541-814-2	Sequence 2, Appli
84	156	9.7	1343	6	US-10-541-814-15	Sequence 15, Appl
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92	154.5	9.6	4390	7	US-11-169-041-169	Sequence 169, App
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108	146.5	9.1	1093	6	US-10-453-372-1088	Sequence 1088, Ap
109	145.5	9.1	1193	7	US-11-139-435-3	Sequence 3, Appli
110	145.5	9.1	1649	6	US-10-995-561-974	Sequence 974, App
111	145.5	9.1	1709	6	US-10-995-561-973	Sequence 973, App
112	145.5	9.1	1709	6	US-10-453-372-410	Sequence 410, App
113	145	9.0	325	6	US-10-311-822-11	Sequence 11, Appl
114	145	9.0	707	6	US-10-453-372-998	Sequence 998, App
115	145	9.0	712	6	US-10-453-372-1000	Sequence 1000, Ap
116	145	9.0	1700	6	US-10-453-372-398	Sequence 398, App
117	145	9.0	1700	6	US-10-453-372-412	Sequence 412, App
118	145	9.0	1700	6	US-10-453-372-414	Sequence 414, App
119	145	9.0	1700	6	US-10-453-372-416	Sequence 416, App
120	145	9.0	1700	6	US-10-453-372-418	Sequence 418, App
121	145	9.0	1902	6	US-10-453-372-1004	Sequence 1004, Ap
122	144.5	9.0	686	7	US-11-051-724-46	Sequence 46, Appl
123	144	9.0	662	6	US-10-493-909-80	Sequence 80, Appl
125	143.5	8.9	398	6	US-10-973-115B-348	Sequence 348, App
128	143.5	8.9	398	7	US-11-290-153-348	Sequence 348, App
129	143.5	8.9	1694	7	US-11-135-855-36	Sequence 36, Appl
130	143.5	8.9	1709	7	US-11-135-855-35	Sequence 35, Appl
131	143	8.9	325	6	US-10-311-822-12	Sequence 12, Appl
132	143	8.9	346	7	US-11-050-857-553	Sequence 553, App
133	143	8.9	346	7	US-11-051-720-1383	Sequence 1383, Ap
134	143	8.9	569	7	US-11-050-857-552	Sequence 552, App
135	143	8.9	569	7	US-11-051-720-1382	Sequence 1382, Ap
136	143	8.9	702	7	US-11-033-039-282	Sequence 282, App
137	143	8.9	702	7	US-11-097-224B-2	Sequence 2, Appli

138	143	8.9	702	7	US-11-050-857-549	Sequence 549, App	221	132.5	8.3	767	7	US-11-043-693-2	Sequence 2, Appl1
139	143	8.9	702	7	US-11-051-720-1451	Sequence 1451, App	222	132.5	8.3	1306	6	US-10-995-561-905	Sequence 905, App
140	143	8.9	702	7	US-11-097-252A-2	Sequence 2, Appl1	223	132.5	8.3	1356	6	US-10-995-561-904	Sequence 904, App
141	143	8.9	719	7	US-11-050-857-551	Sequence 551, App	224	132.5	8.3	1356	6	US-10-995-561-906	Sequence 906, App
142	143	8.9	719	7	US-11-051-720-1381	Sequence 1381, App	225	131.5	8.2	344	6	US-10-973-115B-376	Sequence 376, App
147	142.5	8.9	1191	7	US-11-139-435-2	Sequence 2, Appl1	235	131.5	8.2	344	6	US-11-290-153-376	Sequence 376, App
148	142	8.8	702	6	US-10-510-101-68	Sequence 68, Appl	236	131.5	8.2	555	6	US-10-453-372-764	Sequence 764, App
149	142	8.8	727	6	US-10-995-561-864	Sequence 864, App	237	131.5	8.2	500	6	US-10-453-372-502	Sequence 502, App
150	142	8.8	782	6	US-10-995-561-861	Sequence 861, App	238	130.5	8.1	429	7	US-11-093-274-37	Sequence 37, Appl
151	142	8.8	847	6	US-10-995-561-863	Sequence 863, App	239	130	8.1	357	6	US-10-453-372-760	Sequence 760, App
152	142	8.8	847	6	US-10-995-561-865	Sequence 865, App	240	130	8.1	473	6	US-10-453-372-684	Sequence 684, App
153	142	8.8	847	6	US-10-501-841-61	Sequence 61, Appl	245	130	8.1	765	7	US-11-172-410-19	Sequence 19, Appl
154	141	8.8	488	6	US-10-995-561-860	Sequence 860, App	246	129.5	8.1	283	6	US-10-453-372-850	Sequence 850, App
155	140.5	8.8	961	6	US-10-453-372-726	Sequence 726, App	247	128	8.0	245	6	US-10-115-609-2	Sequence 2, Appl1
156	140.5	8.8	961	6	US-10-453-372-728	Sequence 728, App	248	128	8.0	421	7	US-11-051-724-100	Sequence 100, App
157	140.5	8.8	967	6	US-10-453-372-712	Sequence 712, App	249	127.5	7.9	543	7	US-10-453-372-756	Sequence 756, App
158	140.5	8.8	967	6	US-10-453-372-714	Sequence 714, App	250	127.5	7.9	766	7	US-10-453-372-752	Sequence 752, App
159	140.5	8.8	2591	6	US-10-453-372-718	Sequence 718, App	251	127	7.9	504	7	US-11-186-541-3	Sequence 3, Appl1
160	140.5	8.8	2602	6	US-10-453-372-716	Sequence 716, App	252	127	7.9	504	7	US-11-051-720-1699	Sequence 1699, App
161	140.5	8.8	2617	6	US-10-453-372-666	Sequence 666, App	253	127	7.9	504	7	US-11-051-720-1700	Sequence 1700, App
162	140.5	8.8	2617	6	US-10-453-372-732	Sequence 732, App	254	127	7.9	504	7	US-11-043-806-500	Sequence 500, App
163	140.5	8.8	2617	6	US-10-453-372-734	Sequence 734, App	255	127	7.9	504	7	US-11-043-806-501	Sequence 501, App
164	140.5	8.8	2617	6	US-10-453-372-736	Sequence 736, App	256	127	7.9	584	7	US-11-051-720-324	Sequence 324, App
165	140.5	8.8	2617	6	US-10-453-372-738	Sequence 738, App	257	127	7.9	584	7	US-11-043-806-368	Sequence 368, App
166	140.5	8.8	2617	6	US-10-453-372-740	Sequence 740, App	258	126.5	7.9	419	6	US-10-821-234-1664	Sequence 1664, App
167	140.5	8.8	2617	6	US-10-453-372-742	Sequence 742, App	259	126.5	7.9	419	6	US-10-948-716-4	Sequence 4, Appl1
168	140.5	8.8	2617	6	US-10-453-372-744	Sequence 744, App	260	126.5	7.9	419	6	US-10-948-716-7	Sequence 7, Appl1
169	140.5	8.8	2617	6	US-10-453-372-746	Sequence 746, App	261	126.5	7.9	1433	7	US-11-094-519A-40	Sequence 40, Appl
170	140.5	8.8	2617	6	US-10-453-372-748	Sequence 748, App	262	126	7.9	319	6	US-10-453-372-296	Sequence 296, App
171	140.5	8.8	2617	6	US-10-453-372-750	Sequence 750, App	263	126	7.9	758	7	US-11-043-693-1	Sequence 1, Appl1
172	140	8.7	346	7	US-11-050-857-554	Sequence 554, App	264	126	7.9	1338	6	US-10-821-234-1622	Sequence 1622, App
173	140	8.7	346	7	US-11-051-720-1384	Sequence 1384, App	265	126	7.9	1338	6	US-11-109-156-23	Sequence 23, Appl
174	139.5	8.7	1150	7	US-11-139-435-1	Sequence 1, Appl1	266	126	7.9	1338	7	US-11-075-047A-2	Sequence 2, Appl1
175	139	8.7	457	6	US-10-453-372-686	Sequence 686, App	267	126	7.9	2630	7	US-11-186-731-2	Sequence 2, Appl1
176	139	8.7	457	6	US-10-453-372-690	Sequence 690, App	273	125.5	7.8	282	7	US-11-102-240-60	Sequence 60, Appl
177	139	8.7	460	6	US-10-453-372-688	Sequence 688, App	274	125.5	7.8	282	7	US-11-103-195-60	Sequence 60, Appl
178	139	8.7	473	6	US-10-453-372-692	Sequence 692, App	275	125.5	7.8	458	6	US-10-453-372-786	Sequence 786, App
179	139	8.7	473	6	US-10-453-372-694	Sequence 694, App	276	125.5	7.8	464	6	US-10-453-372-772	Sequence 772, App
180	139	8.7	473	6	US-10-453-372-696	Sequence 696, App	277	125.5	7.8	464	6	US-10-453-372-774	Sequence 774, App
181	139	8.7	473	6	US-10-453-372-698	Sequence 698, App	278	125.5	7.8	473	6	US-10-453-372-770	Sequence 770, App
182	139	8.7	650	7	US-11-072-512-3395	Sequence 3395, App	279	125.5	7.8	1256	6	US-10-493-909-90	Sequence 90, Appl
183	139	8.7	652	6	US-10-453-372-722	Sequence 722, App	280	125	7.8	213	6	US-10-948-716-11	Sequence 11, Appl
184	139	8.7	652	6	US-10-453-372-724	Sequence 724, App	281	125	7.8	302	7	US-11-264-096-2151	Sequence 1151, App
185	139	8.7	670	6	US-10-453-372-670	Sequence 670, App	282	125	7.8	1192	6	US-10-745-586-130	Sequence 130, App
186	139	8.7	670	6	US-10-453-372-682	Sequence 682, App	283	124	7.7	307	6	US-10-453-372-298	Sequence 298, App
187	139	8.7	670	6	US-10-453-372-710	Sequence 710, App	284	124	7.7	309	6	US-10-453-372-302	Sequence 302, App
188	139	8.7	686	6	US-10-453-372-680	Sequence 680, App	285	124	7.7	309	6	US-10-453-372-306	Sequence 306, App
189	139	8.7	977	7	US-11-093-274-39	Sequence 39, Appl	286	124	7.7	315	6	US-10-453-372-290	Sequence 290, App
190	136	8.5	347	6	US-10-453-372-490	Sequence 490, App	287	124	7.7	319	6	US-10-453-372-292	Sequence 292, App
191	136	8.5	347	6	US-10-453-372-500	Sequence 500, App	288	124	7.7	320	6	US-10-453-372-312	Sequence 312, App
192	136	8.5	347	6	US-10-537-002-85	Sequence 85, Appl	289	124	7.7	325	6	US-10-453-372-286	Sequence 286, App
193	136	8.5	500	6	US-10-453-372-492	Sequence 492, App	290	124	7.7	325	6	US-10-453-372-294	Sequence 294, App
194	136	8.5	500	6	US-10-453-372-504	Sequence 504, App	291	124	7.7	336	6	US-10-453-372-308	Sequence 308, App
195	136	8.5	500	7	US-11-102-240-84	Sequence 84, Appl	292	124	7.7	336	6	US-10-453-372-310	Sequence 310, App
196	136	8.5	500	7	US-11-103-195-84	Sequence 84, Appl	293	124	7.7	336	6	US-10-453-372-314	Sequence 314, App
197	135.5	8.4	548	6	US-10-453-372-754	Sequence 754, App	294	124	7.7	344	6	US-10-453-372-284	Sequence 284, App
198	135.5	8.4	548	6	US-10-453-372-768	Sequence 768, App	295	123.5	7.7	345	6	US-10-453-372-758	Sequence 758, App
199	134.5	8.4	290	6	US-10-453-372-836	Sequence 836, App	296	123.5	7.7	426	6	US-10-948-716-1	Sequence 1, Appl1
200	134.5	8.4	290	6	US-10-453-372-842	Sequence 842, App	297	123	7.7	302	6	US-10-453-372-780	Sequence 780, App
201	134.5	8.4	290	6	US-10-453-372-848	Sequence 848, App	298	123	7.7	302	6	US-10-453-372-782	Sequence 782, App
202	134.5	8.4	290	6	US-10-115-609-4	Sequence 4, Appl1	299	123	7.7	302	6	US-10-453-372-788	Sequence 788, App
203	134.5	8.4	290	7	US-11-113-424-77	Sequence 77, Appl	300	123	7.7	442	6	US-10-821-234-1584	Sequence 1584, App
204	134.5	8.4	290	7	US-11-245-713-1	Sequence 1, Appl1	301	123	7.7	490	7	US-11-051-720-325	Sequence 325, App
205	134.5	8.4	290	7	US-11-264-096-763	Sequence 763, App	302	123	7.7	490	7	US-11-043-806-369	Sequence 369, App
206	134.5	8.4	295	6	US-10-453-372-840	Sequence 840, App	303	123	7.7	740	7	US-11-137-465-61	Sequence 61, Appl
207	134.5	8.4	295	6	US-10-453-372-842	Sequence 842, App	304	123	7.7	1250	7	US-11-137-465-62	Sequence 62, Appl
208	134.5	8.4	295	6	US-10-453-372-848	Sequence 848, App	305	122.5	7.6	1571	7	US-11-134-587B-12	Sequence 12, Appl
209	134.5	8.4	290	7	US-11-113-424-77	Sequence 77, Appl	306	122.5	7.6	1571	7	US-11-134-587B-13	Sequence 13, Appl
210	134.5	8.4	290	7	US-11-245-713-1	Sequence 1, Appl1	307	122.5	7.6	1910	7	US-11-134-587B-2	Sequence 2, Appl1
211	134.5	8.4	290	7	US-11-264-096-763	Sequence 763, App	308	122.5	7.6	1910	7	US-11-134-587B-3	Sequence 3, Appl1
212	134.5	8.4	295	6	US-10-453-372-840	Sequence 840, App	309	122	7.6	1252	6	US-10-493-909-89	Sequence 89, Appl
213	134	8.3	860	7	US-11-172-410-2	Sequence 2, Appl1	310	121.5	7.6	424	6	US-10-948-716-6	Sequence 6, Appl1
214	133	8.3	582	7	US-11-051-724-94	Sequence 94, Appl	311	121.5	7.6	428	6	US-10-948-716-3	Sequence 3, Appl1
215	133	8.3	734	7	US-11-093-274-40	Sequence 40, Appl							
216	133	8.3	1315	6	US-10-453-372-1034	Sequence 1034, App							
217	133	8.3	1335	6	US-10-453-372-1030	Sequence 1030, App							
218	132.5	8.3	764	7	US-11-104-110-8	Sequence 8, Appl1							
219	132.5	8.3	764	7	US-11-104-111-28	Sequence 28, Appl							
220	132.5	8.3	764	7	US-11-075-047A-4	Sequence 4, Appl1							

312	121	7.5	245	7	US-11-264-096-762	Sequence 762, App	404	110	6.9	1461	7	US-11-183-136-28	Sequence 28, Appl
313	121	7.5	284	6	US-10-453-372-790	Sequence 790, App	405	109.5	6.8	77	7	US-11-113-424-189	Sequence 189, App
314	121	7.5	290	6	US-10-453-372-776	Sequence 776, App	416	109.5	6.8	466	7	US-11-102-240-104	Sequence 104, App
315	121	7.5	336	6	US-10-453-372-282	Sequence 282, App	417	109.5	6.8	466	7	US-11-103-195-104	Sequence 104, App
316	121	7.5	336	6	US-10-453-372-318	Sequence 318, App	418	109.5	6.8	529	7	US-11-186-541-1	Sequence 1, Appl
317	121	7.5	515	7	US-11-093-374-38	Sequence 38, Appl	419	109	6.8	342	7	US-11-094-519A-39	Sequence 39, Appl
318	121	7.5	822	7	US-11-072-175-254	Sequence 254, App	420	109	6.8	365	7	US-11-087-177-5	Sequence 5, Appl
319	120.5	7.5	327	7	US-11-233-798-2	Sequence 2, Appl	421	109	6.8	466	6	US-10-979-095-1	Sequence 1, Appl
320	120	7.5	319	6	US-10-453-372-300	Sequence 300, App	422	109	6.8	619	7	US-11-072-512-2048	Sequence 2048, Ap
322	120	7.5	321	6	US-11-159-919-2	Sequence 2, Appl	423	109	6.8	895	7	US-11-072-512-2946	Sequence 2946, Ap
323	120	7.5	335	6	US-10-948-716-5	Sequence 5, Appl	424	109	6.8	917	6	US-10-493-909-87	Sequence 87, Appl
324	120	7.5	399	7	US-11-159-919-4	Sequence 4, Appl	425	108.5	6.8	316	7	US-11-264-096-2152	Sequence 2152, Ap
325	120	7.5	399	7	US-11-264-096-1236	Sequence 1236, Ap	426	108.5	6.8	381	7	US-11-197-038-3	Sequence 3, Appl
326	120	7.5	399	7	US-11-264-096-1237	Sequence 1237, Ap	427	108.5	6.8	381	7	US-11-197-038-3	Sequence 3, Appl
327	120	7.5	822	7	US-11-183-567A-2	Sequence 2, Appl	428	108.5	6.8	382	7	US-11-197-038-2	Sequence 2, Appl
328	120	7.5	1745	7	US-11-264-096-2222	Sequence 2222, Ap	429	108.5	6.8	382	7	US-11-197-038-2	Sequence 2, Appl
329	119.5	7.4	297	6	US-10-453-372-766	Sequence 766, App	430	108.5	6.8	404	7	US-11-197-038-1	Sequence 1, Appl
330	119.5	7.4	1299	7	US-11-169-041-231	Sequence 231, App	431	108.5	6.8	404	7	US-11-186-422-2	Sequence 2, Appl
331	119	7.4	266	6	US-10-995-561-544	Sequence 544, App	432	108.5	6.8	404	7	US-11-005-843-1	Sequence 1, Appl
332	119	7.4	291	7	US-11-217-995-10	Sequence 10, Appl	433	108.5	6.8	404	7	US-11-197-644-1	Sequence 1, Appl
333	119	7.4	310	7	US-11-217-995-11	Sequence 11, Appl	435	108.5	6.8	450	6	US-10-973-115B-378	Sequence 378, App
335	119	7.4	1007	6	US-10-329-258-23	Sequence 23, Appl	438	108.5	6.8	450	6	US-11-290-153-378	Sequence 378, App
336	118.5	7.4	317	7	US-11-217-995-9	Sequence 9, Appl	439	108.5	6.8	636	6	US-10-453-372-324	Sequence 324, App
337	118.5	7.4	317	7	US-11-217-995-30	Sequence 30, Appl	440	108.5	6.8	636	6	US-10-453-372-336	Sequence 336, App
338	118.5	7.4	739	6	US-10-493-909-69	Sequence 69, App	441	108.5	6.8	636	6	US-10-453-372-346	Sequence 346, App
339	118.5	7.4	739	6	US-11-107-028-6	Sequence 6, Appl	442	108.5	6.8	636	6	US-10-453-372-354	Sequence 354, App
341	118.5	7.4	1119	6	US-10-973-115B-352	Sequence 352, App	443	108.5	6.8	636	6	US-10-453-372-356	Sequence 356, App
344	118.5	7.4	1119	7	US-11-290-153-352	Sequence 352, App	444	108.5	6.8	636	6	US-10-453-372-366	Sequence 366, App
345	118	7.4	302	6	US-10-453-372-792	Sequence 792, App	445	108.5	6.8	700	6	US-10-453-372-326	Sequence 326, App
346	118	7.4	336	6	US-10-453-372-316	Sequence 316, App	446	108.5	6.8	717	7	US-11-050-857-954	Sequence 954, App
347	118	7.4	421	7	US-11-051-724-96	Sequence 96, Appl	447	108.5	6.8	717	7	US-11-051-720-1695	Sequence 1695, Ap
348	118	7.4	421	7	US-11-051-724-98	Sequence 98, Appl	448	108.5	6.8	757	6	US-10-453-372-320	Sequence 320, App
349	118	7.4	1189	6	US-10-821-234-1209	Sequence 1209, Ap	449	108.5	6.8	757	6	US-10-453-372-350	Sequence 350, App
350	116.5	7.3	267	6	US-10-995-561-543	Sequence 543, App	450	108.5	6.8	757	6	US-10-453-372-328	Sequence 328, App
351	116.5	7.3	424	6	US-10-948-716-10	Sequence 10, Appl	451	108.5	6.8	757	6	US-10-453-372-334	Sequence 334, App
352	116.5	7.3	426	6	US-10-948-716-9	Sequence 9, Appl	452	108.5	6.8	841	6	US-10-857-780-20	Sequence 20, Appl
353	116.5	7.3	602	6	US-10-493-909-51	Sequence 51, Appl	453	108.5	6.8	924	6	US-10-493-909-67	Sequence 67, Appl
355	116	7.2	332	6	US-10-973-115B-386	Sequence 386, App	454	108.5	6.8	924	6	US-11-107-028-26	Sequence 26, Appl
359	116	7.2	332	6	US-11-290-153-386	Sequence 386, App	455	108.5	6.8	1237	6	US-10-501-035-312	Sequence 312, App
360	116	7.2	336	6	US-10-453-372-304	Sequence 304, App	456	108	6.7	238	6	US-10-496-284-15	Sequence 15, Appl
361	116	7.2	2828	7	US-11-080-991-54	Sequence 54, Appl	457	108	6.7	391	6	US-10-996-628-2	Sequence 2, Appl
362	116	7.2	2828	7	US-11-186-284-49	Sequence 49, Appl	458	108	6.7	696	6	US-10-453-372-368	Sequence 368, App
363	115.5	7.2	63	7	US-11-019-711-128	Sequence 128, App	459	108	6.7	712	7	US-11-264-096-1856	Sequence 1856, Ap
364	115.5	7.2	517	7	US-11-051-720-1432	Sequence 1432, Ap	460	108	6.7	713	6	US-10-453-372-322	Sequence 322, App
365	115	7.2	222	6	US-10-453-372-844	Sequence 844, App	461	108	6.7	757	6	US-10-453-372-352	Sequence 352, App
366	115	7.2	235	6	US-10-453-372-784	Sequence 784, App	462	108	6.7	773	6	US-10-453-372-348	Sequence 348, App
367	115	7.2	236	6	US-10-496-284-62	Sequence 62, Appl	463	108	6.7	778	6	US-10-453-372-330	Sequence 330, App
373	115	7.2	917	6	US-10-493-909-75	Sequence 75, Appl	464	107.5	6.7	334	6	US-11-072-512-3119	Sequence 3119, Ap
374	115	7.2	912	6	US-10-493-909-76	Sequence 76, Appl	465	107.5	6.7	334	6	US-10-453-372-332	Sequence 332, App
375	115	7.2	1298	7	US-11-076-427A-12	Sequence 12, Appl	466	107.5	6.7	469	6	US-10-453-372-344	Sequence 344, App
376	115	7.2	1298	7	US-11-075-047A-6	Sequence 6, Appl	467	107	6.7	236	6	US-10-496-284-58	Sequence 58, Appl
377	115	7.2	1362	7	US-11-043-693-33	Sequence 33, Appl	468	106.5	6.6	1493	7	US-11-183-136-26	Sequence 26, Appl
378	115	7.2	1363	7	US-11-076-427A-10	Sequence 10, Appl	469	106	6.6	315	7	US-11-050-857-550	Sequence 550, App
379	115	7.2	1363	7	US-11-075-407A-121	Sequence 121, App	470	106	6.6	315	7	US-11-051-720-1380	Sequence 1380, Ap
380	115	7.2	1368	7	US-11-043-693-34	Sequence 34, Appl	471	105.5	6.6	592	7	US-11-135-855-24	Sequence 24, Appl
381	114.5	7.1	426	6	US-10-821-234-1585	Sequence 1585, Ap	472	105.5	6.6	696	6	US-10-453-372-358	Sequence 358, App
382	114.5	7.1	535	6	US-10-821-234-1015	Sequence 1015, Ap	473	105.5	6.6	696	6	US-10-453-372-364	Sequence 364, App
383	114.5	7.1	1363	7	US-11-043-693-32	Sequence 32, Appl	474	105.5	6.6	817	6	US-10-453-372-520	Sequence 520, App
384	113.5	7.1	349	7	US-11-235-776A-13	Sequence 13, Appl	475	104.5	6.5	259	7	US-11-072-512-2303	Sequence 2303, Ap
385	113.5	7.1	628	7	US-11-080-991-108	Sequence 108, App	476	104.5	6.5	777	7	US-11-043-693-3	Sequence 3, Appl
386	113.5	7.1	647	7	US-11-080-991-32	Sequence 32, Appl	477	104	6.5	270	7	US-11-233-798-23	Sequence 23, Appl
387	113	7.0	253	6	US-10-453-372-288	Sequence 288, App	478	104	6.5	346	6	US-11-235-776A-5	Sequence 5, Appl
389	113	7.0	708	6	US-10-511-538-229	Sequence 229, App	479	104	6.5	696	6	US-10-453-372-362	Sequence 362, App
394	112.5	7.0	288	7	US-11-029-188-2	Sequence 2, Appl	480	103.5	6.4	214	6	US-10-453-372-498	Sequence 498, App
395	112.5	7.0	558	6	US-10-714-995-46	Sequence 46, Appl	481	103.5	6.4	334	7	US-11-072-175-156	Sequence 156, App
396	112	7.0	354	7	US-11-072-512-2965	Sequence 2965, Ap	483	103.5	6.4	477	6	US-10-973-115B-50	Sequence 50, Appl
397	112	7.0	879	7	US-11-051-724-90	Sequence 90, Appl	486	103.5	6.4	477	7	US-11-290-153-50	Sequence 50, Appl
398	112	7.0	1189	7	US-11-050-857-953	Sequence 953, App	487	103.5	6.4	696	6	US-10-453-372-360	Sequence 360, App
399	112	7.0	1189	7	US-11-051-720-1694	Sequence 1694, Ap	488	103	6.4	31	7	US-11-050-857-1141	Sequence 1141, Ap
400	111.5	6.9	256	7	US-11-050-857-58	Sequence 58, Appl	489	103	6.4	31	7	US-11-051-720-1773	Sequence 1773, Ap
401	111.5	6.9	487	7	US-11-050-857-253	Sequence 253, App	490	103	6.4	133	7	US-11-072-512-3128	Sequence 3128, Ap
402	110	6.9	309	6	US-10-453-372-778	Sequence 778, App	491	103	6.4	201	7	US-11-050-857-161	Sequence 161, App
403	110	6.9	577	6	US-10-493-909-66	Sequence 66, Appl	492	103	6.4	201	7	US-11-051-720-1301	Sequence 1301, Ap

494	103	6.4	428	6	US-10-973-115B-292	Sequence 292, App	577	96	6.0	388	6	US-10-503-590A-28	Sequence 28, Appl
497	103	6.4	428	7	US-11-290-153-292	Sequence 292, App	579	96	6.0	394	6	US-10-973-115B-520	Sequence 520, App
498	103	6.4	488	6	US-10-016-686-3	Sequence 3, Appli	587	96	6.0	394	7	US-11-290-153-520	Sequence 520, App
499	102.5	6.4	255	6	US-10-514-534-8	Sequence 8, Appli	588	96	6.0	899	6	US-10-453-372-506	Sequence 506, App
500	102.5	6.4	261	6	US-10-861-227-7	Sequence 7, Appli	589	96	6.0	899	6	US-10-453-372-524	Sequence 524, App
501	102.5	6.4	409	6	US-10-821-234-892	Sequence 892, App	590	96	6.0	899	6	US-10-453-372-526	Sequence 526, App
502	102.5	6.4	551	7	US-11-235-776A-7	Sequence 7, Appli	591	96	6.0	899	6	US-10-453-372-528	Sequence 528, App
503	102.5	6.4	584	7	US-11-072-175-157	Sequence 157, App	592	96	6.0	899	6	US-10-453-372-530	Sequence 530, App
504	102	6.4	335	6	US-10-948-716-2	Sequence 2, Appli	593	96	6.0	899	6	US-10-453-372-532	Sequence 532, App
505	101.5	6.3	308	7	US-11-235-776A-1	Sequence 1, Appli	594	96	6.0	899	6	US-10-453-372-534	Sequence 534, App
506	101.5	6.3	316	7	US-11-197-038-6	Sequence 6, Appli	595	96	6.0	899	6	US-10-453-372-536	Sequence 536, App
507	101.5	6.3	316	7	US-11-197-644-6	Sequence 6, Appli	596	96	6.0	899	6	US-10-453-372-538	Sequence 538, App
508	101.5	6.3	317	7	US-11-197-038-5	Sequence 5, Appli	597	96	6.0	899	6	US-10-453-372-540	Sequence 540, App
509	101.5	6.3	317	7	US-11-197-644-5	Sequence 5, Appli	598	96	6.0	899	6	US-10-453-372-542	Sequence 542, App
510	101.5	6.3	321	7	US-11-186-422-8	Sequence 8, Appli	599	96	6.0	899	6	US-10-453-372-544	Sequence 544, App
511	101.5	6.3	334	6	US-10-689-742-134	Sequence 134, App	600	96	6.0	899	6	US-10-453-372-546	Sequence 546, App
512	101.5	6.3	339	7	US-11-197-038-4	Sequence 4, Appli	605	95.5	6.0	269	6	US-10-821-234-1308	Sequence 1308, Ap
513	101.5	6.3	339	7	US-11-005-843-2	Sequence 2, Appli	606	95.5	6.0	304	7	US-11-087-177-4	Sequence 4, Appli
514	101.5	6.3	339	7	US-11-197-644-4	Sequence 4, Appli	607	95.5	6.0	331	7	US-11-264-096-1917	Sequence 1917, Ap
515	101.5	6.3	316	7	US-11-185-436-20	Sequence 20, Appl	622	95.5	6.0	405	6	US-10-311-822-9	Sequence 9, Appli
516	101.5	6.3	516	7	US-11-186-422-6	Sequence 6, Appli	623	95.5	6.0	409	6	US-11-264-096-1503	Sequence 1503, Ap
517	101.5	6.3	548	7	US-11-235-776A-3	Sequence 3, Appli	624	95.5	6.0	425	6	US-10-311-822-4	Sequence 4, Appli
518	101.5	6.3	551	7	US-11-235-776A-9	Sequence 9, Appli	626	95.5	6.0	708	6	US-10-973-115B-298	Sequence 298, App
519	101	6.3	406	7	US-11-000-463-177	Sequence 377, App	629	95.5	6.0	708	7	US-11-290-153-298	Sequence 298, App
520	101	6.3	406	7	US-11-000-463-849	Sequence 849, App	630	95.5	6.0	738	6	US-10-995-561-692	Sequence 692, App
521	101	6.3	814	7	US-10-079-463-9513	Sequence 9513, Ap	631	95.5	6.0	738	6	US-10-995-561-693	Sequence 693, App
522	100.5	6.3	187	6	US-10-204-639-3	Sequence 3, Appli	632	95	5.9	88	6	US-10-948-571-61	Sequence 61, Appl
523	100.5	6.3	230	6	US-10-115-609-23	Sequence 23, Appl	633	95	5.9	402	7	US-11-174-150-47	Sequence 47, Appl
524	100.5	6.3	290	7	US-11-113-424-78	Sequence 78, Appl	634	95	5.9	407	7	US-11-072-512-3074	Sequence 3074, Ap
525	100.5	6.3	290	7	US-11-245-713-3	Sequence 3, Appli	635	95	5.9	412	6	US-10-204-639-43	Sequence 43, Appl
526	100.5	6.3	640	6	US-10-917-905-4	Sequence 4, Appli	636	95	5.9	748	6	US-10-821-234-1479	Sequence 1479, Ap
527	100	6.2	282	7	US-11-186-284-85	Sequence 85, Appl	637	94.5	5.9	474	7	US-11-075-047A-20	Sequence 20, Appl
528	99.5	6.2	281	6	US-10-055-877-125	Sequence 125, App	638	94.5	5.9	533	7	US-11-147-047-33	Sequence 33, Appl
529	99.5	6.2	281	6	US-10-055-877-262	Sequence 262, App	639	94.5	5.9	570	7	US-11-075-047A-8	Sequence 8, Appli
530	99.5	6.2	281	7	US-11-087-177-17	Sequence 17, Appl	640	94.5	5.9	583	7	US-11-075-047A-125	Sequence 125, App
531	99.5	6.2	640	6	US-10-917-905-1	Sequence 1, Appli	641	94.5	5.9	583	7	US-11-075-047A-128	Sequence 128, App
532	99.5	6.2	640	6	US-10-973-115B-368	Sequence 368, App	642	94.5	5.9	771	7	US-11-147-047-34	Sequence 34, Appl
533	99.5	6.2	640	7	US-11-290-153-368	Sequence 368, App	643	94	5.9	235	6	US-10-453-372-406	Sequence 406, App
537	99	6.2	281	7	US-11-087-177-3	Sequence 3, Appli	644	94	5.9	235	6	US-10-453-372-408	Sequence 408, App
538	99	6.2	341	6	US-10-514-534-6	Sequence 6, Appli	645	94	5.9	238	7	US-11-177-648-39	Sequence 39, Appl
539	99	6.2	388	6	US-10-503-590A-4	Sequence 4, Appli	646	94	5.9	239	6	US-10-453-372-400	Sequence 400, App
540	99	6.2	833	6	US-10-453-372-518	Sequence 518, App	647	94	5.9	239	6	US-10-453-372-402	Sequence 402, App
541	98	6.1	330	6	US-10-453-372-516	Sequence 516, App	648	94	5.9	239	6	US-10-453-372-404	Sequence 404, App
542	98	6.1	336	6	US-10-453-372-510	Sequence 510, App	649	94	5.9	305	6	US-10-055-877-126	Sequence 126, App
543	98	6.1	337	7	US-11-050-857-392	Sequence 392, App	650	94	5.9	305	6	US-10-055-877-264	Sequence 264, App
544	98	6.1	434	7	US-11-204-709-24	Sequence 24, Appl	651	94	5.9	305	7	US-11-080-091-2	Sequence 2, Appli
545	98	6.1	501	7	US-11-173-893-10	Sequence 10, Appl	652	94	5.9	305	7	US-11-087-177-7	Sequence 7, Appli
546	98	6.1	583	7	US-11-080-991-64	Sequence 64, Appl	653	93.5	5.8	239	6	US-10-496-284-11	Sequence 11, Appl
547	98	6.1	788	7	US-11-173-893-2	Sequence 2, Appli	654	93.5	5.8	239	7	US-11-264-096-133	Sequence 133, App
548	98	6.1	898	6	US-10-624-932-2	Sequence 2, Appli	655	93.5	5.8	766	7	US-11-147-047-27	Sequence 27, Appl
549	98	6.1	898	6	US-10-453-372-514	Sequence 514, App	656	93.5	5.8	898	6	US-10-453-372-522	Sequence 522, App
550	98	6.1	898	7	US-11-183-136-14	Sequence 14, Appl	657	93	5.8	285	5	US-09-978-360A-489	Sequence 489, App
551	97.5	6.1	59	5	US-09-978-360A-676	Sequence 676, App	658	93	5.8	945	7	US-11-183-136-18	Sequence 18, Appl
552	97.5	6.1	169	6	US-10-453-372-838	Sequence 838, App	659	93	5.8	1084	6	US-10-517-905-12	Sequence 12, Appl
553	97.5	6.1	178	6	US-10-453-372-846	Sequence 846, App	660	93	5.8	1084	6	US-10-517-905-23	Sequence 23, Appl
554	97.5	6.1	282	6	US-10-055-877-127	Sequence 127, App	661	93	5.8	1085	6	US-10-517-905-6	Sequence 6, Appli
555	97.5	6.1	282	7	US-11-087-177-9	Sequence 9, Appli	662	93	5.8	1086	6	US-10-517-905-8	Sequence 8, Appli
556	97.5	6.1	326	6	US-11-233-798-6	Sequence 6, Appli	663	93	5.8	1089	6	US-10-517-905-2	Sequence 2, Appli
557	97.5	6.1	422	6	US-10-917-905-3	Sequence 3, Appli	664	93	5.8	1089	6	US-10-517-905-4	Sequence 4, Appli
558	97	6.0	335	6	US-10-453-372-512	Sequence 512, App	665	93	5.8	1089	6	US-10-517-905-21	Sequence 21, Appl
559	97	6.0	488	7	US-11-235-776A-11	Sequence 11, App	666	93	5.8	1089	6	US-10-517-905-25	Sequence 25, Appl
560	97	6.0	548	6	US-10-493-909-78	Sequence 78, Appl	667	93	5.8	1089	6	US-10-517-905-27	Sequence 27, Appl
561	96.5	6.0	146	7	US-11-050-857-1136	Sequence 1136, Ap	668	93	5.8	1089	7	US-11-148-770-32	Sequence 32, Appl
567	96.5	6.0	468	7	US-11-264-096-2260	Sequence 2260, Ap	669	93	5.8	1089	7	US-11-076-427A-14	Sequence 14, Appl
568	96	6.0	192	6	US-10-514-534-9	Sequence 9, Appli	670	93	5.8	1089	7	US-11-075-047A-117	Sequence 117, App
569	96	6.0	333	7	US-11-197-038-37	Sequence 37, Appl	671	93	5.8	1089	7	US-11-177-894-26	Sequence 26, Appl
570	96	6.0	323	7	US-11-197-644-37	Sequence 37, Appl	672	93	5.8	1089	7	US-11-177-894-27	Sequence 27, Appl
571	96	6.0	334	7	US-11-197-038-36	Sequence 36, Appl	673	93	5.8	1089	7	US-11-177-894-28	Sequence 28, Appl
572	96	6.0	324	7	US-11-197-644-36	Sequence 36, Appl	674	93	5.8	1089	7	US-11-177-894-29	Sequence 29, Appl
573	96	6.0	331	6	US-10-453-372-508	Sequence 508, App	675	93	5.8	1089	7	US-11-233-510-28	Sequence 28, Appl
574	96	6.0	338	7	US-11-124-367A-471	Sequence 471, App	676	93	5.8	1090	6	US-10-517-905-10	Sequence 10, Appl
575	96	6.0	346	7	US-11-197-038-35	Sequence 35, Appl	677	93	5.8	1451	6	US-10-995-561-829	Sequence 829, App
576	96	6.0	346	7	US-11-197-644-35	Sequence 35, Appl	678	92.5	5.8	548	7	US-11-137-465-47	Sequence 47, Appl

679	92.5	5.8	550	6	US-10-453-372-76	Sequence 76, Appl	768	87	5.4	416	6	US-10-453-372-1028	Sequence 1028, Ap
680	92.5	5.8	578	6	US-10-453-372-66	Sequence 66, Appl	769	87	5.4	438	6	US-11-186-541-2	Sequence 2, Appl
681	92.5	5.8	578	6	US-10-453-372-80	Sequence 80, Appl	770	87	5.4	448	6	US-10-453-372-1024	Sequence 1024, Ap
682	92	5.7	101	6	US-10-821-234-1061	Sequence 1061, Ap	771	87	5.4	451	6	US-10-453-372-1040	Sequence 1040, Ap
683	92	5.7	238	7	US-11-177-648-35	Sequence 35, Appl	772	87	5.4	456	6	US-10-453-372-1026	Sequence 1026, Ap
684	92	5.7	238	7	US-11-177-648-36	Sequence 36, Appl	773	87	5.4	456	6	US-10-453-372-1026	Sequence 1026, Ap
685	92	5.7	238	7	US-11-177-648-37	Sequence 37, Appl	774	87	5.4	488	6	US-10-453-372-1038	Sequence 1038, Ap
686	92	5.7	238	7	US-11-177-648-80	Sequence 80, Appl	775	86.5	5.4	503	6	US-10-453-372-1038	Sequence 1038, Ap
687	92	5.7	370	7	US-11-052-554A-120	Sequence 120, App	776	86.5	5.4	170	6	US-10-861-227-10	Sequence 10, Appl
688	92	5.7	551	7	US-11-000-463-346	Sequence 346, App	777	86.5	5.4	430	7	US-11-016-503-17	Sequence 17, Appl
689	91.5	5.7	203	7	US-11-197-038-18	Sequence 18, Appl	778	86.5	5.4	444	7	US-11-043-788-311	Sequence 311, App
690	91.5	5.7	203	7	US-11-197-038-18	Sequence 18, Appl	779	86.5	5.4	458	7	US-11-016-503-12	Sequence 12, Appl
691	91.5	5.7	204	7	US-11-197-038-17	Sequence 17, Appl	780	86.5	5.4	458	7	US-11-089-803-2	Sequence 2, Appl
692	91.5	5.7	204	7	US-11-197-038-17	Sequence 17, Appl	781	86.5	5.4	458	7	US-11-218-234-2	Sequence 2, Appl
693	91.5	5.7	228	7	US-11-197-038-20	Sequence 20, Appl	782	86.5	5.4	458	6	US-11-204-709-6	Sequence 6, Appl
694	91.5	5.7	228	7	US-11-197-038-20	Sequence 20, Appl	783	86.5	5.4	532	6	US-10-595-561-897	Sequence 897, App
695	91.5	5.7	228	7	US-11-197-038-19	Sequence 19, Appl	784	86.5	5.4	532	6	US-10-493-909-2	Sequence 2, Appl
696	91.5	5.7	229	7	US-11-197-038-19	Sequence 19, Appl	785	86	5.4	532	7	US-10-493-909-2	Sequence 308, App
697	91.5	5.7	238	7	US-11-197-038-17	Sequence 17, Appl	786	86	5.4	219	6	US-10-487-324A-11	Sequence 11, Appl
698	91.5	5.7	398	6	US-10-996-628-4	Sequence 4, Appl	787	86	5.4	219	7	US-11-224-623-11	Sequence 11, Appl
699	91.5	5.7	398	7	US-11-223-492-6	Sequence 6, Appl	788	86	5.4	301	6	US-10-055-877-124	Sequence 124, App
700	91.5	5.7	438	7	US-11-186-422-10	Sequence 10, Appl	789	86	5.4	301	6	US-10-055-877-261	Sequence 261, App
701	91.5	5.7	438	7	US-11-197-038-34	Sequence 34, Appl	790	86	5.4	301	7	US-11-000-463-752	Sequence 752, App
702	91.5	5.7	438	7	US-11-197-038-34	Sequence 34, Appl	791	86	5.4	354	7	US-11-087-177-37	Sequence 37, Appl
703	91.5	5.7	439	7	US-11-197-038-33	Sequence 33, Appl	792	86	5.4	575	6	US-11-051-720-1324	Sequence 1324, Ap
704	91.5	5.7	439	7	US-11-197-038-33	Sequence 33, Appl	793	86	5.4	1822	7	US-10-453-372-78	Sequence 78, Appl
705	91.5	5.7	461	7	US-11-197-038-32	Sequence 32, Appl	794	85.5	5.3	170	6	US-11-169-041-193	Sequence 193, App
706	91.5	5.7	461	7	US-11-197-038-32	Sequence 32, Appl	795	85.5	5.3	189	6	US-10-861-227-6	Sequence 6, Appl
707	91	5.7	264	6	US-10-218-325-14	Sequence 14, Appl	796	85.5	5.3	189	6	US-10-453-372-338	Sequence 338, App
708	91	5.7	384	7	US-11-000-463-804	Sequence 804, App	797	85.5	5.3	189	6	US-10-453-372-340	Sequence 340, App
709	91	5.7	384	7	US-11-000-463-805	Sequence 805, App	798	85.5	5.3	215	6	US-10-453-372-342	Sequence 342, App
710	91	5.7	384	7	US-11-000-463-806	Sequence 806, App	799	85.5	5.3	356	7	US-10-236-051-4	Sequence 4, Appl
711	91	5.7	384	7	US-11-000-463-807	Sequence 807, App	800	85.5	5.3	371	7	US-11-087-099-2981	Sequence 2981, Ap
712	91	5.7	440	7	US-11-166-496-2	Sequence 2, Appl	801	85.5	5.3	619	7	US-11-075-047A-30	Sequence 30, Appl
713	91	5.7	963	7	US-11-183-136-16	Sequence 16, Appl	802	85.5	5.3	619	7	US-11-087-099-396	Sequence 396, App
714	90.5	5.6	832	7	US-11-045-004-41	Sequence 41, Appl	803	85	5.3	238	6	US-11-087-099-12020	Sequence 12020, A
715	90	5.6	33	7	US-11-050-857-1065	Sequence 1065, Ap	804	85	5.3	242	7	US-10-496-284-19	Sequence 19, Appl
716	90	5.6	238	7	US-11-177-648-38	Sequence 38, Appl	805	85	5.3	268	6	US-11-259-232-42	Sequence 42, Appl
717	90	5.6	238	7	US-11-177-648-40	Sequence 40, Appl	806	85	5.3	301	7	US-10-218-325-13	Sequence 13, Appl
718	90	5.6	409	6	US-10-503-590A-2	Sequence 2, Appl	807	85	5.3	374	6	US-11-087-177-35	Sequence 35, Appl
719	89.5	5.6	199	7	US-11-264-096-131	Sequence 131, App	808	85	5.3	374	6	US-10-246-019A-4	Sequence 4, Appl
720	89.5	5.6	354	6	US-10-986-405-278	Sequence 278, App	809	85	5.3	374	7	US-11-000-463-453	Sequence 453, App
721	89.5	5.6	500	7	US-11-072-512-2825	Sequence 2825, Ap	810	85	5.3	2013	7	US-11-299-182-20	Sequence 20, Appl
722	89.5	5.6	537	6	US-10-493-909-74	Sequence 74, Appl	811	84.5	5.3	171	6	US-10-973-115B-356	Sequence 356, App
723	89	5.5	535	6	US-10-973-115B-124	Sequence 124, App	812	84.5	5.3	171	6	US-10-986-405-331	Sequence 331, App
724	89	5.5	535	6	US-10-973-115B-124	Sequence 124, App	813	84.5	5.3	171	6	US-10-986-405-331	Sequence 356, App
725	88.5	5.5	240	7	US-11-239-510-11	Sequence 11, Appl	814	84.5	5.3	247	7	US-11-290-153-356	Sequence 356, App
726	88.5	5.5	716	6	US-11-147-047-52	Sequence 52, Appl	815	84.5	5.3	363	7	US-10-857-780-18	Sequence 18, Appl
727	88.5	5.5	716	7	US-11-142-867-2	Sequence 2, Appl	816	84.5	5.3	332	6	US-10-493-909-63	Sequence 63, Appl
728	88.5	5.5	716	7	US-11-290-153-512	Sequence 512, App	817	84.5	5.3	332	7	US-11-104-812-2	Sequence 2, Appl
729	88.5	5.5	716	7	US-10-401-386B-34	Sequence 34, Appl	818	84.5	5.3	332	7	US-11-105-279-2	Sequence 2, Appl
730	88.5	5.5	255	6	US-10-517-696-143	Sequence 143, App	819	84.5	5.3	332	7	US-11-107-028-22	Sequence 22, Appl
731	88	5.5	255	6	US-10-517-696-143	Sequence 143, App	820	84.5	5.3	332	7	US-11-043-788-307	Sequence 307, App
732	88	5.5	454	6	US-10-453-372-1022	Sequence 1022, App	821	84.5	5.3	332	7	US-10-995-561-785	Sequence 785, App
733	88.5	5.5	458	7	US-11-016-503-16	Sequence 16, Appl	822	84.5	5.3	532	6	US-10-995-561-787	Sequence 65, Appl
734	88	5.5	458	7	US-11-089-803-6	Sequence 6, Appl	823	84.5	5.3	532	6	US-10-493-909-65	Sequence 114, App
735	88	5.5	458	7	US-11-149-728-2	Sequence 2, Appl	824	84.5	5.3	532	6	US-10-501-841-114	Sequence 24, Appl
736	88	5.5	458	7	US-11-149-728-2	Sequence 2, Appl	825	84.5	5.3	532	7	US-11-107-028-24	Sequence 1102, Ap
737	88	5.5	458	7	US-11-149-728-2	Sequence 2, Appl	826	84.5	5.3	532	7	US-10-821-234-1102	Sequence 12160, A
738	88.5	5.5	458	7	US-11-193-746-2	Sequence 2, Appl	827	84.5	5.3	532	7	US-11-087-099-12160	Sequence 19, Appl
739	88.5	5.5	458	7	US-11-218-234-6	Sequence 6, Appl	828	84.5	5.3	532	7	US-11-045-004-19	Sequence 2764, Ap
740	88.5	5.5	458	7	US-10-784-004-643	Sequence 643, App	829	84.5	5.3	532	7	US-11-072-512-2764	Sequence 10, Appl
741	88	5.5	477	6	US-10-784-004-693	Sequence 693, App	830	84.5	5.3	532	7	US-11-233-798-10	Sequence 34, Appl
742	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	831	84.5	5.3	532	7	US-11-177-648-34	Sequence 2068, Ap
743	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	832	84.5	5.3	532	7	US-11-054-515-2068	Sequence 2068, Ap
744	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	833	84.5	5.3	532	7	US-11-266-444-2068	Sequence 1325, Ap
745	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	834	84.5	5.3	532	7	US-11-055-877-77	Sequence 77, Appl
746	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	835	84.5	5.3	532	7	US-11-188-298-10330	Sequence 10330, A
747	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	836	84.5	5.3	532	7		
748	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	837	84	5.2	106	7		
749	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	838	84	5.2	194	7		
750	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	839	84	5.2	238	7		
751	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	840	84	5.2	246	7		
752	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	841	84	5.2	246	7		
753	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	842	84	5.2	352	7		
754	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	843	84	5.2	401	6		
755	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	844	84	5.2	409	7		
756	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	845	84	5.2				
757	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	846	84	5.2				
758	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	847	84	5.2				
759	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	848	84	5.2				
760	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	849	84	5.2				
761	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	850	84	5.2				
762	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	851	84	5.2				
763	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	852	84	5.2				
764	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	853	84	5.2				
765	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	854	84	5.2				
766	88	5.5	477	6	US-10-784-004-1047	Sequence 1047, Ap	855	84	5.2				
767	88	5.5	477	6	US-10-784								

844	84	5.2	479	7	US-11-147-047-44	Sequence 44, Appl	951	80.5	5.0	618	7	US-11-087-099-5108	Sequence 5108, Ap
859	84	5.2	628	6	US-10-453-372-548	Sequence 548, App	952	80	5.0	278	7	US-11-192-123-2	Sequence 2, Appli
860	84	5.2	628	6	US-10-453-372-550	Sequence 550, App	953	80	5.0	462	7	US-11-177-648-9	Sequence 9, Appli
861	84	5.2	628	6	US-11-147-047-45	Sequence 45, Appl	954	80	5.0	535	6	US-10-493-909-84	Sequence 84, Appl
862	84	5.2	650	7	US-11-299-182-2	Sequence 2, Appli	956	80	5.0	653	6	US-10-917-905-2	Sequence 2, Appli
863	84	5.2	651	7	US-11-198-819-22	Sequence 22, Appl	957	80	5.0	653	6	US-10-973-115B-438	Sequence 438, App
864	84	5.2	652	7	US-11-299-182-4	Sequence 4, Appli	960	80	5.0	653	7	US-11-135-855-25	Sequence 25, Appl
865	83.5	5.2	170	6	US-10-861-227-5	Sequence 5, Appli	961	80	5.0	653	7	US-11-290-153-438	Sequence 438, App
867	83.5	5.2	335	6	US-10-982-357-2	Sequence 2, Appli	962	80	5.0	718	7	US-11-045-004-1498	Sequence 1498, Ap
872	83.5	5.2	335	6	US-10-501-841-2	Sequence 2, Appli	963	80	5.0	945	7	US-11-019-711-121	Sequence 121, App
873	83.5	5.2	335	7	US-11-102-240-46	Sequence 46, Appl	964	79.5	5.0	137	6	US-10-821-234-1701	Sequence 1701, Ap
874	83.5	5.2	335	7	US-11-240-769-59	Sequence 59, Appl	965	79.5	5.0	218	7	US-11-194-989-37	Sequence 37, Appl
875	83.5	5.2	335	7	US-11-103-195-46	Sequence 46, Appl	966	79.5	5.0	218	7	US-11-195-207-37	Sequence 37, Appl
876	83.5	5.2	347	7	US-11-282-853-8	Sequence 8, Appli	967	79.5	5.0	224	6	US-10-982-357-84	Sequence 84, Appl
877	83.5	5.2	358	6	US-10-821-234-1563	Sequence 1563, Ap	973	79.5	5.0	237	6	US-10-884-730-357	Sequence 357, App
878	83.5	5.2	388	7	US-11-045-004-36	Sequence 36, Appl	974	79.5	5.0	253	7	US-11-259-232-44	Sequence 44, Appl
879	83.5	5.2	398	6	US-10-821-234-1583	Sequence 1583, Ap	975	79.5	5.0	295	7	US-11-169-041-139	Sequence 139, App
880	83.5	5.2	447	6	US-10-884-730-379	Sequence 379, App	976	79.5	5.0	295	7	US-11-072-175-146	Sequence 146, App
881	83.5	5.2	448	7	US-11-299-182-18	Sequence 18, Appl	977	79.5	5.0	305	6	US-10-821-234-1449	Sequence 1449, Ap
882	83.5	5.2	467	6	US-10-246-019A-2	Sequence 2, Appli	978	79.5	5.0	305	6	US-10-501-841-87	Sequence 87, Appl
883	83.5	5.2	467	7	US-11-000-463-452	Sequence 452, App	979	79.5	5.0	322	6	US-10-979-095-8	Sequence 8, Appli
884	83.5	5.2	467	7	US-11-000-463-924	Sequence 924, App	980	79.5	5.0	330	7	US-11-072-512-3524	Sequence 3524, Ap
885	83.5	5.2	467	7	US-11-000-463-925	Sequence 925, App	981	79.5	5.0	341	7	US-11-072-512-3424	Sequence 3424, Ap
886	83	5.2	240	6	US-10-866-530-1	Sequence 1, Appli	982	79.5	5.0	343	7	US-11-087-099-7263	Sequence 7263, Ap
887	83	5.2	301	7	US-11-000-463-280	Sequence 280, App	983	79.5	5.0	419	6	US-10-506-454-973	Sequence 973, App
888	83	5.2	613	7	US-11-166-594-4	Sequence 4, Appl	984	79.5	5.0	515	7	US-11-051-724-92	Sequence 92, Appl
889	83	5.2	917	7	US-11-144-987-20	Sequence 20, Appl	985	79.5	5.0	972	6	US-10-821-234-1587	Sequence 1587, Ap
890	83	5.2	917	7	US-11-205-935-20	Sequence 20, Appl	986	79.5	5.0	2314	7	US-11-097-728-2	Sequence 2, Appli
891	83	5.2	917	6	US-10-861-227-12	Sequence 12, Appl	987	79.5	5.0	2353	7	US-11-097-728-6	Sequence 6, Appli
892	82.5	5.1	170	6	US-11-086-289-4	Sequence 4, Appli	988	79	4.9	51	7	US-11-264-096-816	Sequence 816, App
893	82.5	5.1	236	7	US-11-113-424-80	Sequence 80, Appl	989	79	4.9	176	7	US-11-184-147-4	Sequence 4, Appli
894	82.5	5.1	334	7	US-11-282-853-6	Sequence 6, Appli	990	79	4.9	219	7	US-11-194-989-12	Sequence 12, Appl
895	82.5	5.1	351	7	US-11-045-004-16	Sequence 16, Appl	991	79	4.9	219	7	US-11-195-207-12	Sequence 12, Appl
896	82.5	5.1	439	7	US-10-493-909-82	Sequence 82, Appl	992	79	4.9	244	7	US-11-054-515-2058	Sequence 2058, Ap
897	82.5	5.1	447	6	US-11-113-424-81	Sequence 81, Appl	993	79	4.9	244	7	US-11-266-444-2058	Sequence 2058, Ap
898	82.5	5.1	527	7	US-11-144-987-6	Sequence 6, Appli	994	79	4.9	346	7	US-11-174-150-33	Sequence 33, Appl
899	82.5	5.1	902	7	US-11-205-935-6	Sequence 6, Appli	995	79	4.9	432	6	US-10-995-561-738	Sequence 738, App
900	82.5	5.1	902	7	US-11-145-861-338	Sequence 338, App	996	79	4.9	666	6	US-10-981-356A-29	Sequence 29, Appl
901	82	5.1	17	7	US-10-496-284-9	Sequence 9, Appli	997	79	4.9	667	7	US-11-096-046-29	Sequence 29, Appl
902	82	5.1	205	6	US-10-821-234-1575	Sequence 1575, Ap	998	79	4.9	934	7	US-11-046-653-4	Sequence 4, Appli
903	82	5.1	365	6	US-10-996-568A-12273	Sequence 12273, A	1000	79	4.9	945	6	US-10-973-115B-146	Sequence 146, App
904	82	5.1	404	7	US-11-096-568A-12272	Sequence 12272, A	1003	79	4.9	945	7	US-11-019-711-38	Sequence 38, Appl
905	82	5.1	411	7	US-11-096-568A-12272	Sequence 12271, A	1004	79	4.9	945	7	US-11-183-136-20	Sequence 20, Appl
906	82	5.1	447	7	US-11-096-568A-12271	Sequence 29, Appl	1005	79	4.9	945	7	US-11-290-153-146	Sequence 146, App
907	82	5.1	707	6	US-10-204-639-29	Sequence 1, Appli	1006	79	4.9	1684	7	US-11-188-298-16493	Sequence 16493, A
908	81.5	5.1	214	7	US-11-173-564-1	Sequence 15, Appl	1007	78.5	4.9	119	6	US-10-993-543-170	Sequence 170, App
909	81.5	5.1	214	7	US-11-208-422-15	Sequence 2039, Ap	1008	78.5	4.9	132	6	US-10-489-866-30	Sequence 30, Appl
924	81.5	5.1	214	7	US-11-264-096-2039	Sequence 3787, Ap	1009	78.5	4.9	237	7	US-11-054-515-2112	Sequence 2112, Ap
925	81	5.0	158	7	US-11-072-512-3787	Sequence 9, Appli	1010	78.5	4.9	237	7	US-11-266-444-2112	Sequence 2112, Ap
926	81	5.0	172	6	US-10-861-227-9	Sequence 2, Appli	1011	78.5	4.9	234	7	US-11-128-551-7	Sequence 7, Appli
927	81	5.0	176	7	US-11-184-147-2	Sequence 9, Appli	1012	78.5	4.9	343	7	US-11-087-099-7151	Sequence 7151, Ap
928	81	5.0	215	6	US-10-374-954-9	Sequence 9, Appli	1017	78.5	4.9	545	6	US-10-493-909-86	Sequence 86, Appl
929	81	5.0	455	7	US-11-016-503-14	Sequence 14, Appl	1018	78.5	4.9	648	6	US-10-917-905-6	Sequence 6, Appli
930	81	5.0	455	7	US-11-089-803-4	Sequence 4, Appli	1019	78.5	4.9	666	6	US-10-981-356A-30	Sequence 30, Appl
931	81	5.0	455	7	US-11-218-234-4	Sequence 4, Appli	1020	78.5	4.9	931	7	US-11-079-463-8401	Sequence 8401, Ap
932	81	5.0	455	7	US-11-204-709-10	Sequence 10, Appl	1021	78.5	4.9	1813	6	US-10-495-083-10	Sequence 10, Appl
933	81	5.0	484	6	US-10-784-004-322	Sequence 322, App	1022	78.5	4.9	149	7	US-11-089-266-2	Sequence 2, Appli
934	81	5.0	484	6	US-10-784-004-372	Sequence 372, App	1023	78	4.9	239	7	US-11-177-648-10	Sequence 10, Appl
935	81	5.0	484	6	US-10-784-004-906	Sequence 906, App	1024	78	4.9	273	6	US-10-517-696-124	Sequence 124, App
936	81	5.0	484	6	US-10-784-004-930	Sequence 930, App	1025	78	4.9	276	6	US-10-251-567-1	Sequence 1, Appli
937	81	5.0	698	7	US-11-079-463-6720	Sequence 6720, Ap	1026	78	4.9	667	7	US-11-096-046-30	Sequence 30, Appl
938	81	5.0	742	7	US-11-072-512-2476	Sequence 2476, Ap	1027	77.5	4.8	109	7	US-11-049-536-340	Sequence 340, App
939	81	5.0	1100	7	US-11-079-463-6319	Sequence 6319, Ap	1029	77.5	4.8	114	7	US-11-199-739-340	Sequence 340, App
940	81	5.0	1155	6	US-10-793-626-1780	Sequence 11, Appl	1029	77.5	4.8	114	7	US-11-037-199-34	Sequence 34, Appl
941	80.5	5.0	170	6	US-10-861-227-11	Sequence 79, Appl	1030	77.5	4.8	211	6	US-10-236-051-8	Sequence 19, Appl
942	80.5	5.0	224	6	US-10-982-357-79	Sequence 2036, Ap	1031	77.5	4.8	214	7	US-11-208-422-19	Sequence 19, Appl
943	80.5	5.0	237	7	US-11-054-515-2036	Sequence 2036, Ap	1032	77.5	4.8	226	7	US-11-183-205-42	Sequence 42, Appl
944	80.5	5.0	264	6	US-11-266-444-2036	Sequence 138, App	1033	77.5	4.8	229	7	US-11-226-788-2	Sequence 2, Appli
945	80.5	5.0	266	6	US-10-517-696-138	Sequence 79, Appl	1034	77.5	4.8	237	6	US-10-884-730-120	Sequence 120, App
946	80.5	5.0	266	6	US-10-884-730-79	Sequence 165, App	1035	77.5	4.8	237	6	US-10-884-730-359	Sequence 359, App
947	80.5	5.0	266	6	US-10-884-730-165	Sequence 165, App	1036	77.5	4.8	247	7	US-11-054-515-1764	Sequence 1764, Ap
948	80.5	5.0	266	6	US-10-884-730-166	Sequence 166, App	1037	77.5	4.8	247	7	US-11-266-444-1764	Sequence 1764, Ap
949	80.5	5.0	329	7	US-11-029-188-4	Sequence 4, Appli	1037	77.5	4.8	266	6	US-10-884-730-115	Sequence 116, App
950	80.5	5.0	595	7	US-11-264-096-2258	Sequence 2258, Ap	1038	77.5	4.8				

1039	77.5	4.8	265	6	US-10-884-730-121	Sequence 121, App	1116	76	4.7	131	7	US-11-259-232-35	Sequence 35, Appl
1040	77.5	4.8	266	7	US-11-000-463-853	Sequence 853, App	1117	76	4.7	218	7	US-11-072-512-3286	Sequence 3286, Ap
1041	77.5	4.8	284	7	US-11-072-512-3648	Sequence 853, App	1118	76	4.7	235	7	US-11-128-900-14	Sequence 14, Appl
1042	77.5	4.8	338	6	US-10-821-234-1565	Sequence 1565, Ap	1119	76	4.7	235	7	US-11-128-900-65	Sequence 65, Appl
1043	77.5	4.8	411	6	US-10-453-632-74	Sequence 74, Appl	1120	76	4.7	250	7	US-11-054-515-1529	Sequence 1529, Ap
1044	77.5	4.8	416	7	US-11-226-657-136	Sequence 136, App	1121	76	4.7	250	7	US-11-266-444-1529	Sequence 1529, Ap
1045	77.5	4.8	424	6	US-10-453-372-68	Sequence 68, Appl	1122	76	4.7	259	6	US-10-512-184-34	Sequence 34, Appl
1046	77.5	4.8	435	7	US-11-204-709-19	Sequence 19, Appl	1123	76	4.7	274	7	US-11-192-123-19	Sequence 19, Appl
1047	77.5	4.8	444	7	US-11-029-003-16	Sequence 16, Appl	1124	76	4.7	371	6	US-10-512-184-71	Sequence 71, Appl
1048	77.5	4.8	522	7	US-11-072-512-2664	Sequence 2664, Ap	1125	76	4.7	381	6	US-10-515-872-12	Sequence 12, Appl
1049	77.5	4.8	530	6	US-10-858-730-232	Sequence 232, App	1126	76	4.7	626	6	US-10-512-184-49	Sequence 49, Appl
1050	77.5	4.8	544	6	US-10-493-909-73	Sequence 73, Appl	1127	76	4.7	1043	7	US-11-079-463-9606	Sequence 9606, Ap
1051	77.5	4.8	902	7	US-11-144-987-8	Sequence 8, Appl	1128	75.5	4.7	112	7	US-11-155-843-192	Sequence 192, App
1052	77.5	4.8	902	7	US-11-205-935-8	Sequence 8, Appl	1129	75.5	4.7	214	7	US-11-128-900-71	Sequence 71, Appl
1053	77.5	4.8	915	7	US-11-144-987-16	Sequence 16, Appl	1130	75.5	4.7	239	7	US-11-271-090-4	Sequence 4, Appl
1054	77.5	4.8	915	7	US-11-144-987-22	Sequence 22, Appl	1131	75.5	4.7	249	7	US-11-054-515-974	Sequence 974, App
1055	77.5	4.8	915	7	US-11-205-935-16	Sequence 16, Appl	1132	75.5	4.7	249	7	US-11-266-444-974	Sequence 974, App
1056	77.5	4.8	915	7	US-11-205-935-22	Sequence 22, Appl	1133	75.5	4.7	250	7	US-11-239-510-15	Sequence 15, Appl
1057	77.5	4.8	917	7	US-11-144-987-24	Sequence 24, Appl	1134	75.5	4.7	252	6	US-10-401-3868-38	Sequence 38, Appl
1058	77.5	4.8	917	7	US-11-144-987-26	Sequence 26, Appl	1135	75.5	4.7	253	7	US-11-239-510-17	Sequence 17, Appl
1059	77.5	4.8	917	7	US-11-205-935-24	Sequence 24, Appl	1136	75.5	4.7	278	7	US-11-233-798-12	Sequence 12, Appl
1060	77.5	4.8	917	7	US-11-205-935-26	Sequence 26, Appl	1137	75.5	4.7	288	6	US-10-821-234-1062	Sequence 1062, Ap
1061	77.5	4.8	2044	7	US-11-045-004-7	Sequence 7, Appl	1138	75.5	4.7	328	6	US-10-595-561-884	Sequence 884, App
1062	77.5	4.8	5291	7	US-11-052-554A-281	Sequence 281, App	1139	75.5	4.7	812	7	US-11-072-512-2027	Sequence 2027, App
1063	77	4.8	28	7	US-11-264-096-958	Sequence 958, App	1140	75.5	4.7	885	7	US-11-096-568A-30498	Sequence 30498, A
1064	77	4.8	91	7	US-11-197-038-12	Sequence 12, Appl	1141	75.5	4.7	910	7	US-11-144-987-2	Sequence 2, Appl
1065	77	4.8	91	7	US-11-197-644-12	Sequence 12, Appl	1142	75.5	4.7	910	7	US-11-205-935-2	Sequence 2, Appl
1066	77	4.8	112	7	US-11-072-512-3016	Sequence 3016, Ap	1143	75.5	4.7	911	7	US-11-096-568A-30497	Sequence 30497, A
1067	77	4.8	119	7	US-11-264-096-317	Sequence 317, App	1144	75.5	4.7	1552	7	US-11-108-459-2	Sequence 2, Appl
1068	77	4.8	244	7	US-11-072-512-3205	Sequence 3205, Ap	1145	75.5	4.7	1597	7	US-11-210-471-13	Sequence 13, Appl
1069	77	4.8	280	7	US-11-159-919-8	Sequence 8, Appl	1146	75.5	4.7	1678	7	US-11-124-367A-340	Sequence 340, App
1070	77	4.8	280	7	US-11-032-773-957	Sequence 957, App	1147	75.5	4.7	1678	7	US-11-124-367A-341	Sequence 341, App
1071	77	4.8	333	7	US-11-079-463-8468	Sequence 8468, Ap	1148	75	4.7	153	5	US-09-978-360A-490	Sequence 490, App
1072	77	4.8	331	7	US-11-203-526-40	Sequence 40, Appl	1149	75	4.7	215	6	US-10-973-1158-488	Sequence 488, App
1073	77	4.8	483	7	US-11-239-510-19	Sequence 19, Appl	1150	75	4.7	215	6	US-10-573-1158-488	Sequence 488, App
1074	77	4.8	548	6	US-10-493-909-77	Sequence 77, Appl	1151	75	4.7	215	7	US-11-080-591-112	Sequence 112, App
1075	77	4.8	1120	7	US-11-079-463-9538	Sequence 9538, Ap	1152	75	4.7	250	7	US-11-290-153-488	Sequence 488, App
1076	76.5	4.8	165	7	US-11-188-298-15023	Sequence 15023, A	1153	75	4.7	250	7	US-11-054-515-899	Sequence 899, App
1077	76.5	4.8	217	6	US-10-644-807-256	Sequence 256, App	1154	75	4.7	297	6	US-11-266-444-899	Sequence 899, App
1078	76.5	4.8	218	7	US-11-004-590-229	Sequence 229, App	1155	75	4.7	297	6	US-10-453-372-70	Sequence 70, Appl
1079	76.5	4.8	224	6	US-10-982-357-82	Sequence 82, Appl	1156	75	4.7	323	7	US-11-096-568A-19741	Sequence 19741, A
1080	76.5	4.8	236	7	US-11-086-289-8	Sequence 8, Appl	1157	75	4.7	355	7	US-11-096-568A-19740	Sequence 19740, A
1081	76.5	4.8	237	6	US-10-884-730-12	Sequence 12, Appl	1158	75	4.7	414	7	US-11-096-568A-19739	Sequence 19739, A
1082	76.5	4.8	237	6	US-10-884-730-12	Sequence 12, Appl	1159	75	4.7	495	7	US-11-264-096-1679	Sequence 1679, Ap
1083	76.5	4.8	237	6	US-10-884-730-360	Sequence 360, App	1160	75	4.7	495	7	US-11-264-096-1680	Sequence 1680, Ap
1084	76.5	4.8	231	6	US-10-218-325-10	Sequence 10, Appl	1161	75	4.7	517	6	US-10-517-696-144	Sequence 144, App
1085	76.5	4.8	278	6	US-10-218-325-6	Sequence 6, Appl	1162	75	4.7	606	6	US-10-624-932-16	Sequence 16, Appl
1086	76.5	4.8	294	6	US-10-055-877-128	Sequence 128, App	1163	75	4.7	606	6	US-10-624-932-18	Sequence 18, Appl
1087	76.5	4.8	307	6	US-10-055-877-263	Sequence 263, App	1164	75	4.7	648	7	US-11-079-463-9537	Sequence 9537, Ap
1088	76.5	4.8	308	7	US-11-079-463-10276	Sequence 10276, A	1165	75	4.7	1102	7	US-11-079-463-9537	Sequence 9537, Ap
1089	76.5	4.8	336	7	US-11-113-424-83	Sequence 83, Appl	1166	75	4.7	1106	7	US-11-076-427A-16	Sequence 16, Appl
1090	76.5	4.8	348	7	US-11-229-769-211	Sequence 211, App	1167	75	4.7	1106	7	US-11-075-047A-119	Sequence 119, App
1091	76.5	4.8	348	7	US-11-229-769-368	Sequence 368, App	1168	74.5	4.6	1106	7	US-11-264-096-1553	Sequence 1553, Ap
1092	76.5	4.8	348	7	US-11-233-798-20	Sequence 20, Appl	1169	74.5	4.6	102	7	US-11-155-843-32	Sequence 32, Appl
1093	76.5	4.8	349	7	US-11-229-769-242	Sequence 242, App	1170	74.5	4.6	108	7	US-11-229-264-4	Sequence 4, Appl
1094	76.5	4.8	379	7	US-11-188-298-15945	Sequence 15945, A	1171	74.5	4.6	111	7	US-11-229-264-2	Sequence 2, Appl
1095	76.5	4.8	388	7	US-11-188-298-1176	Sequence 1176, Ap	1172	74.5	4.6	113	6	US-10-932-334-60	Sequence 60, Appl
1096	76.5	4.8	398	7	US-11-188-298-8864	Sequence 8864, Ap	1173	74.5	4.6	114	7	US-11-037-199-17	Sequence 17, Appl
1097	76.5	4.8	618	6	US-10-512-184-48	Sequence 48, Appl	1174	74.5	4.6	116	7	US-11-065-943-49	Sequence 49, Appl
1098	76.5	4.8	668	7	US-11-087-099-5101	Sequence 5101, Ap	1175	74.5	4.6	131	6	US-10-789-273-14	Sequence 14, Appl
1099	76.5	4.8	671	7	US-11-202-507A-14	Sequence 14, Appl	1176	74.5	4.6	147	6	US-10-496-284-56	Sequence 56, Appl
1100	76.5	4.8	672	7	US-11-202-507A-7	Sequence 7, Appl	1177	74.5	4.6	234	7	US-11-041-095-25	Sequence 25, Appl
1101	76.5	4.8	900	7	US-11-144-987-10	Sequence 10, Appl	1178	74.5	4.6	239	7	US-11-041-095-19	Sequence 19, Appl
1102	76.5	4.8	900	7	US-11-205-935-10	Sequence 10, Appl	1179	74.5	4.6	248	7	US-11-054-515-1995	Sequence 1995, Ap
1103	76.5	4.8	902	7	US-11-144-987-12	Sequence 12, Appl	1180	74.5	4.6	248	7	US-11-266-444-1995	Sequence 1995, Ap
1104	76.5	4.8	902	7	US-11-144-987-14	Sequence 14, Appl	1181	74.5	4.6	249	7	US-11-054-515-1817	Sequence 1817, Ap
1105	76.5	4.8	902	7	US-11-205-935-12	Sequence 12, Appl	1182	74.5	4.6	249	7	US-11-054-515-2049	Sequence 2049, Ap
1106	76.5	4.8	902	7	US-11-205-935-14	Sequence 14, Appl	1183	74.5	4.6	249	7	US-11-266-444-1817	Sequence 1817, Ap
1107	76.5	4.8	921	6	US-10-880-144-2	Sequence 2, Appl	1184	74.5	4.6	249	7	US-11-266-444-2049	Sequence 2049, Ap
1108	76.5	4.8	1152	7	US-11-045-004-37	Sequence 37, Appl	1185	74.5	4.6	266	6	US-10-884-730-295	Sequence 295, App
1109	76	4.7	50	7	US-11-264-096-1266	Sequence 1266, Ap	1186	74.5	4.6	266	6	US-10-884-730-296	Sequence 296, App
1110	76	4.7	104	7	US-11-000-463-939	Sequence 939, App	1187	74.5	4.6	290	7	US-11-041-095-13	Sequence 13, Appl
1111	76	4.7	106	7	US-11-000-463-467	Sequence 467, App	1188	74.5	4.6	303	7	US-11-198-819-2	Sequence 2, Appl
1112	76	4.7					1189	74.5	4.6	328	6	US-10-501-035-333	Sequence 333, App
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1119							1196	74.5	4.6				
1120							1197	74.5	4.6				
1121							1198	74.5	4.6				
1122							1199	74.5	4.6				
1123							1200	74.5	4.6				
1124							1201	74.5	4.6				
1125							1202	74.5	4.6				
1126							1203	74.5	4.6				
1127							1204	74.5	4.6				
1128							1205	74.5	4.6				
1129							1206	74.5	4.6				

1197	74.5	4.6	409	7	US-11-188-298-20382	Sequence 20382, A	1274	73.5	4.6	678	7	US-11-202-507A-11	Sequence 11, Appl
1198	74.5	4.6	434	7	US-11-087-099-11618	Sequence 11618, A	1275	73.5	4.6	679	7	US-11-202-507A-5	Sequence 5, Appl
1199	74.5	4.6	469	7	US-11-096-568A-2376	Sequence 2376, Ap	1276	73.5	4.6	900	7	US-11-144-987-4	Sequence 4, Appl
1200	74.5	4.6	469	7	US-11-096-568A-2378	Sequence 2378, Ap	1277	73.5	4.6	900	7	US-11-205-935-4	Sequence 4, Appl
1201	74.5	4.6	566	6	US-10-467-057-3302	Sequence 3302, Ap	1278	73.5	4.6	1417	7	US-11-052-554A-8	Sequence 8, Appl
1202	74.5	4.6	656	6	US-10-784-004-451	Sequence 451, App	1279	73.5	4.6	2053	7	US-11-013-759-9	Sequence 9, Appl
1203	74.5	4.6	855	7	US-11-087-099-12274	Sequence 12274, A	1280	73	4.5	144	7	US-11-055-163-15	Sequence 15, Appl
1204	74.5	4.6	852	7	US-11-079-463-8461	Sequence 8461, Ap	1281	73	4.5	242	7	US-11-054-515-1830	Sequence 1830, Ap
1205	74.5	4.6	1137	7	US-11-087-099-5799	Sequence 5799, Ap	1282	73	4.5	242	7	US-11-266-444-1830	Sequence 1830, Ap
1206	74.5	4.6	1642	7	US-11-183-261-40	Sequence 40, Appl	1283	73	4.5	244	7	US-11-054-515-1491	Sequence 1491, Ap
1207	74.5	4.6	3396	7	US-11-183-261-39	Sequence 39, Appl	1284	73	4.5	244	7	US-11-266-444-1491	Sequence 1491, Ap
1208	74	4.6	239	7	US-11-086-289-12	Sequence 12, Appl	1285	73	4.5	278	7	US-11-192-123-21	Sequence 21, Appl
1209	74	4.6	241	7	US-11-054-515-1937	Sequence 1937, Ap	1286	73	4.5	333	7	US-11-181-234-5	Sequence 5, Appl
1210	74	4.6	241	7	US-11-266-444-1937	Sequence 1937, Ap	1287	73	4.5	333	7	US-11-181-234-7	Sequence 7, Appl
1211	74	4.6	250	6	US-10-512-184-27	Sequence 27, Appl	1288	73	4.5	353	7	US-11-079-463-5436	Sequence 5436, Ap
1212	74	4.6	252	7	US-11-054-515-1992	Sequence 1992, Ap	1289	73	4.5	353	7	US-11-057-012-65	Sequence 65, Appl
1213	74	4.6	252	7	US-11-266-444-1992	Sequence 1992, Ap	1290	73	4.5	439	7	US-11-198-819-12	Sequence 12, Appl
1214	74	4.6	258	6	US-10-512-184-26	Sequence 26, Appl	1291	73	4.5	439	7	US-11-299-182-8	Sequence 8, Appl
1215	74	4.6	259	6	US-10-873-528-166	Sequence 166, App	1292	73	4.5	508	7	US-11-183-567A-1	Sequence 1, Appl
1216	74	4.6	327	6	US-10-512-184-62	Sequence 62, Appl	1293	73	4.5	565	7	US-11-087-099-7018	Sequence 7018, Ap
1217	74	4.6	327	6	US-10-512-184-64	Sequence 64, Appl	1294	73	4.5	568	6	US-10-714-887-224	Sequence 224, App
1218	74	4.6	328	6	US-10-512-184-63	Sequence 63, Appl	1295	73	4.5	793	7	US-11-045-004-23	Sequence 23, Appl
1219	74	4.6	468	7	US-11-086-289-14	Sequence 14, Appl	1296	73	4.5	1118	7	US-11-079-463-9536	Sequence 9536, Ap
1220	74	4.6	529	7	US-11-113-424-85	Sequence 82, Appl	1298	73	4.5	1184	6	US-10-973-115B-412	Sequence 412, App
1221	74	4.6	576	6	US-10-512-184-65	Sequence 65, Appl	1301	73	4.5	1184	7	US-11-290-153-412	Sequence 412, App
1222	74	4.6	594	7	US-11-072-512-3281	Sequence 3281, Ap	1302	73	4.5	1243	6	US-10-453-372-1136	Sequence 1136, Ap
1223	74	4.6	635	6	US-10-512-184-47	Sequence 47, Appl	1303	72.5	4.5	114	7	US-11-037-199-26	Sequence 26, Appl
1224	74	4.6	931	7	US-11-019-711-117	Sequence 117, App	1304	72.5	4.5	128	7	US-11-264-096-1501	Sequence 1501, Ap
1225	74	4.6	931	7	US-11-183-136-22	Sequence 22, Appl	1305	72.5	4.5	131	7	US-11-012-353-63	Sequence 63, Appl
1226	74	4.6	966	7	US-11-054-281-72	Sequence 72, Appl	1306	72.5	4.5	160	6	US-10-986-408-326	Sequence 326, App
1227	74	4.6	1122	6	US-10-467-657-6112	Sequence 6112, Ap	1307	72.5	4.5	203	7	US-11-062-186-70	Sequence 70, Appl
1228	74	4.6	1574	7	US-11-212-443-179	Sequence 179, App	1308	72.5	4.5	206	7	US-11-062-186-69	Sequence 69, Appl
1229	74	4.6	1978	7	US-11-212-443-60	Sequence 60, Appl	1309	72.5	4.5	208	7	US-11-062-186-63	Sequence 63, Appl
1230	73.5	4.6	113	6	US-10-932-334-8	Sequence 8, Appl	1310	72.5	4.5	213	7	US-11-062-186-67	Sequence 67, Appl
1231	73.5	4.6	113	6	US-10-932-334-58	Sequence 58, Appl	1311	72.5	4.5	214	7	US-11-183-205-55	Sequence 55, Appl
1232	73.5	4.6	113	6	US-10-932-334-82	Sequence 82, Appl	1312	72.5	4.5	224	7	US-11-062-186-64	Sequence 64, Appl
1233	73.5	4.6	113	6	US-10-489-866-20	Sequence 20, Appl	1313	72.5	4.5	229	7	US-11-062-186-68	Sequence 68, Appl
1234	73.5	4.6	114	7	US-11-072-512-3797	Sequence 3797, Ap	1314	72.5	4.5	247	7	US-11-062-186-68	Sequence 62, Appl
1235	73.5	4.6	131	7	US-11-125-837-23	Sequence 23, Appl	1315	72.5	4.5	247	7	US-11-033-039-877	Sequence 877, App
1236	73.5	4.6	132	6	US-10-932-334-50	Sequence 50, Appl	1316	72.5	4.5	249	7	US-11-054-515-2002	Sequence 2002, Ap
1237	73.5	4.6	139	7	US-11-267-310-2	Sequence 2, Appl	1317	72.5	4.5	249	7	US-11-266-444-2002	Sequence 2002, Ap
1238	73.5	4.6	139	7	US-11-267-191-2	Sequence 2, Appl	1318	72.5	4.5	252	7	US-11-062-186-66	Sequence 66, Appl
1239	73.5	4.6	149	7	US-11-050-857-489	Sequence 489, App	1319	72.5	4.5	257	6	US-10-995-561-747	Sequence 747, App
1240	73.5	4.6	149	7	US-11-043-806-371	Sequence 371, App	1320	72.5	4.5	257	6	US-10-496-349B-53	Sequence 53, Appl
1241	73.5	4.6	214	7	US-11-025-712-11	Sequence 11, Appl	1321	72.5	4.5	259	6	US-10-995-561-883	Sequence 883, App
1242	73.5	4.6	236	7	US-11-086-289-20	Sequence 20, Appl	1322	72.5	4.5	266	6	US-10-884-730-1	Sequence 1, Appl
1243	73.5	4.6	237	6	US-10-884-730-22	Sequence 22, Appl	1323	72.5	4.5	266	6	US-10-884-730-4	Sequence 4, Appl
1244	73.5	4.6	237	6	US-10-884-730-358	Sequence 358, App	1324	72.5	4.5	276	7	US-11-038-901-19	Sequence 19, Appl
1245	73.5	4.6	237	7	US-11-054-515-2006	Sequence 2006, Ap	1325	72.5	4.5	307	7	US-11-000-463-332	Sequence 332, App
1246	73.5	4.6	237	7	US-11-266-444-2006	Sequence 2006, Ap	1326	72.5	4.5	312	7	US-11-000-463-334	Sequence 334, App
1247	73.5	4.6	243	7	US-11-054-515-1863	Sequence 1863, Ap	1327	72.5	4.5	331	6	US-10-499-151A-30	Sequence 30, Appl
1248	73.5	4.6	243	7	US-11-266-444-1863	Sequence 1863, Ap	1328	72.5	4.5	339	6	US-10-499-151A-20	Sequence 20, Appl
1249	73.5	4.6	247	7	US-11-054-515-1651	Sequence 1651, Ap	1329	72.5	4.5	341	7	US-11-240-769-72	Sequence 72, Appl
1250	73.5	4.6	247	7	US-11-054-515-1703	Sequence 1703, Ap	1334	72.5	4.5	341	7	US-11-151-868-2	Sequence 2, Appl
1251	73.5	4.6	247	7	US-11-266-444-1651	Sequence 1651, Ap	1335	72.5	4.5	343	7	US-11-087-099-7008	Sequence 7008, Ap
1252	73.5	4.6	247	7	US-11-266-444-1703	Sequence 1703, Ap	1336	72.5	4.5	452	7	US-11-045-004-733	Sequence 733, App
1253	73.5	4.6	262	6	US-10-884-730-289	Sequence 289, App	1337	72.5	4.5	457	6	US-10-995-561-741	Sequence 741, App
1254	73.5	4.6	266	6	US-10-884-730-47	Sequence 47, Appl	1338	72.5	4.5	488	7	US-11-188-298-9576	Sequence 9576, Ap
1255	73.5	4.6	266	6	US-10-884-730-270	Sequence 270, App	1339	72.5	4.5	541	7	US-11-059-814-20	Sequence 20, Appl
1256	73.5	4.6	266	6	US-10-884-730-285	Sequence 285, App	1340	72.5	4.5	629	7	US-11-096-568A-30870	Sequence 30870, A
1257	73.5	4.6	266	6	US-10-884-730-287	Sequence 287, App	1341	72.5	4.5	705	7	US-11-079-463-7483	Sequence 7483, Ap
1258	73.5	4.6	301	7	US-11-188-298-12054	Sequence 12054, A	1342	72.5	4.5	931	7	US-11-019-711-118	Sequence 118, App
1259	73.5	4.6	303	7	US-11-096-568A-33215	Sequence 33215, A	1343	72.5	4.5	931	7	US-11-019-711-119	Sequence 119, App
1260	73.5	4.6	318	7	US-11-179-977-16	Sequence 16, Appl	1344	72.5	4.5	931	7	US-11-019-711-120	Sequence 120, App
1265	73.5	4.6	377	7	US-11-267-310-55	Sequence 55, Appl	1345	72.5	4.5	931	7	US-11-183-136-24	Sequence 24, Appl
1266	73.5	4.6	377	7	US-11-267-191-55	Sequence 55, Appl	1346	72.5	4.5	1392	7	US-11-013-759-3	Sequence 3, Appl
1267	73.5	4.6	383	7	US-11-267-310-57	Sequence 57, Appl	1347	72.5	4.5	1392	7	US-11-013-759-13	Sequence 13, Appl
1268	73.5	4.6	383	7	US-11-267-191-57	Sequence 57, Appl	1348	72.5	4.5	2047	7	US-11-013-759-4	Sequence 4, Appl
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• [श्रीमद्भगवद्गीता / भाष्य / अध्याय १०](#)

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SUMMARIES

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